

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run on: November 9, 2002, 19:42:10 ; Search time 12895 Seconds  
(without alignments)  
11808.133 Million cell updates/sec  
Title: US-09-974-592-3  
Perfect score: 5232  
Sequence: 1 gaaaggtggaagtccta.....tcaaaaaaaaaaaaaaaag 5232  
Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0  
Searched: 2054640 seqs, 14551402878 residues  
Word size : 0  
Total number of hits satisfying chosen parameters: 4109280  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_cm.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_man.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	5232	100.0	5232	6	AR106397	AR106397 Sequence
2	5232	100.0	5232	6	AR116699	AR116699 Sequence
3	3523	67.3	123742	2	HS167P19	Z93014 Homo sapien
4	3523	67.3	133391	9	HS0315G1	AL121601 Human DNA
5	3523	67.3	201197	2	HS424J12	Z82207 Homo sapien
6	2278	43.5	3000	6	AX412131	AX412131 Sequence
7	2027	38.7	2404	6	AX429575	AX429575 Sequence
8	1990	38.0	2540	6	AR103281	AR103281 Sequence
9	1990	38.0	2540	6	AX412118	AX412118 Sequence
10	1990	38.0	2540	6	HSU45880	U45880 Human X-lin
11	1757	33.6	2086	9	BC032729	BC032729 Homo sapi
12	1560	29.8	1659	6	E31042	E31042 Method for
13	1560	29.8	1659	9	HSU32974	U32974 Human IAP-1
14	912	17.4	201197	2	HS424J12	Z82207 Homo sapien
15	146	2.8	158093	9	AL390123	AL390123 Human DNA
16	128	2.4	185771	2	AC111718	AC111718 Rattus no
17	114	2.2	158075	2	AC131311	AC131311 Homo sapi
18	112	2.1	69937	2	AC069566	AC069566 Homo sapi
19	112	2.1	150107	2	AC027582	AC027582 Homo sapi
20	112	2.1	184406	9	AC009476	AC009476 Homo sapi
21	112	2.1	313264	2	AC023053	AC023053 Homo sapi
22	108	2.1	147598	9	AC093503	AC093503 Homo sapi
23	108	2.1	173316	2	AC025983	AC025983 Homo sapi
24	107	2.0	112902	9	AC005230	AC005230 Homo sapi
25	107	2.0	145556	2	CNS07EEU	AL445903 Human chr
26	107	2.0	160653	2	AC026306	AC026306 Homo sapi
27	106	2.0	161381	2	AC120024	AC120024 Homo sapi
28	103	2.0	40271	2	AC090411	AC090411 Homo sapi
29	103	2.0	40328	9	HSAC000021	AC000021 Origins o
30	103	2.0	43795	9	AC000022	AC000022 Genomic s
31	103	2.0	85674	9	AF164343	AF164343 Homo sapi
32	103	2.0	103356	9	AC010089	AC010089 Homo sapi
33	103	2.0	141580	9	AF241729	AF241729 Homo sapi
34	103	2.0	163494	2	AC016964	AC016964 Homo sapi
35	103	2.0	166937	9	AC025679	AC025679 Homo sapi
36	103	2.0	171987	9	AC100757	AC100757 Homo sapi
37	103	2.0	177355	9	AC023310	AC023310 Homo sapi
38	103	2.0	180345	9	AC006983	AC006983 Homo sapi
39	103	2.0	184637	2	AC006990	AC006990 Homo sapi
40	103	2.0	186838	9	AC006338	AC006338 Homo sapi
41	103	2.0	187313	9	AC022212	AC022212 Homo sapi
42	103	2.0	190506	2	AC068990	AC068990 Homo sapi
43	103	2.0	199458	9	AC010088	AC010088 Homo sapi
44	103	2.0	207471	2	AF001401	AF001401 Homo sapi
45	102	1.9	63966	9	AL451141	AL451141 Human DNA

ALIGNMENTS

RESULT 1  
AR106397  
LOCUS  
DEFINITION Sequence 3 from patent US 6107041.  
ACCESSION AR106397  
VERSION AR106397.1 GI:12820927  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5232)  
AUTHORS Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.  
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease

AR106397 5232 bp DNA linear PAT 14-FEB-2001

JOURNAL Patent: US 6107041-A 3 22-AUG-2000;

FEATURES Location/Qualifiers

source 1. 5232

BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others

ORIGIN

Query Match 100.0%; Score 5232; DB 6; Length 5232;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAAAGGTGGACAGTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGGATCT 60

Qy 61 AAAACTCTGTACCTGCAGACATCAATTAAGGAAGAAATTTGTAGAAGAGTTTAATAGA 120

Db 61 AAAACTCTGTACCTGCAGACATCAATTAAGGAAGAAATTTGTAGAAGAGTTTAATAGA 120

Qy 121 TTAATAACTTTTGTCTAAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCAACACTGGCAGGA 180

Db 121 TTAATAACTTTTGTCTAAATTTTCCAAAGTGGTAGTCTCTGTTTCAGCATCAACACTGGCAGGA 180

Qy 181 GCAGGGTTCTTTATACCTGTGAAGGAGATACCGTGCCTGCTTTAGTTGTCATGCAGCT 240

Db 181 GCAGGGTTCTTTATACCTGTGAAGGAGATACCGTGCCTGCTTTAGTTGTCATGCAGCT 240

Qy 241 GTAGATAGATGCAATATGGAGATCAAGCAGTTGGAAGACACAGGAAAGTATCCCAAAAT 300

Db 241 GTAGATAGATGCAATATGGAGATCAAGCAGTTGGAAGACACAGGAAAGTATCCCAAAAT 300

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Db 301 TGCAGATTTATCAAGGGCTTTTATCTTGAAATAGTGCAGCGAGCTACAAAATTTCTGGT 360

Qy 361 ATCCAGATGTCAGTACAAAGTTGAAACTATCTGGAAGACAGAGATCAATTTGCCCTTA 420

Db 361 ATCCAGATGTCAGTACAAAGTTGAAACTATCTGGAAGACAGAGATCAATTTGCCCTTA 420

Qy 421 GACAGGCATCTGACACACATGACAGTATCTTTTGAGAACTGGCGAGTTGTAGATATA 480

Db 421 GACAGGCATCTGACACACATGACAGTATCTTTTGAGAACTGGCGAGTTGTAGATATA 480

Qy 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAGTCC 540

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Db 541 TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600

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Db 1381 TGCAAAATCTGTATGGATAGAAAATTTGCTATCTGTTTTTGTCTTGTGGACATCTAGTC 1440

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Db 1501 TTCAAGCAAAAATTTTATGCTTAATCTAATCTATAGTAGGAGTGTATGTTGTCT 1560

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Db 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTAGTTGGCAATATA 1680

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Db 1681 ATCTTTGAATTTCTTGATTTTCAGGGTATTAGCTGATTAATCCATTTTTTACTGTTA 1740

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Db 1741 TTTAATTTGAAACCATAGACTAAGAAATAAGAACATCATATACTAATACTGAACAAATGCT 1800

Qy 1801 ATTCATAGTACTGATTTAATTTCTAAGTGAATTAATCATCTGGATTTTTAT 1860

Db 1801 ATTCATAGTACTGATTTAATTTCTAAGTGAATTAATCATCTGGATTTTTAT 1860

Qy 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTCTATATAAATGTGGAGATTAGAGTTA 1920

Db 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTCTATATAAATGTGGAGATTAGAGTTA 1920

Qy 1921 ATCTCCCAATCACATAATTTGTTTGTGAAAAAGAAATAAATGTTCCATGCTGTTG 1980

Db 1921 ATCTCCCAATCACATAATTTGTTTGTGAAAAAGAAATAAATGTTCCATGCTGTTG 1980

Qy 1981 GAAAGATAGAGATTGTTTTTGTAGAGGTTGGTGTGTTTTTAGGATTTCTGTCATTTCT 2040

Db 1981 GAAAGATAGAGATTGTTTTTGTAGAGGTTGGTGTGTTTTTAGGATTTCTGTCATTTCT 2040

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QY 2161 AAGATATGTTAAAGTGAAATGCAAGTGCGCAACACACTATGTATGCTGAGCCAGATCA 2220  
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QY 2401 GTATTACTTTTGAATCAGAAATTTTGAAGATATTTTGTCTGCTGCAATTTTTTATAAGTAT 2460  
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QY 2581 TGTGGATGAAAAATATTTCTCAGTGGTAGTTTTTGTACAGGTAGACCATGCTTTATCTTG 2640  
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QY 2701 AATTAATAGTATGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTTCTGATTT 2760  
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QY 3241 AGTTTGAGAGTAAACCTGTAATAAATATATTTTTTGTGTTACTTTCTAAAGAGAAGAGTA 3300  
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QY 3421 CTGGAGTGCAGTGGAGTGATCTCTGCTCAGTCAACCTCCGCCCTTCTGGGTTCAAGCAT 3480  
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QY 3541 ATTTTTTTTTTATTTTTAGTAGAGAGGGGTTTACCATGTTGGCCAGGCTGGTATCAAC 3600  
DB ATTTTTTTTTTATTTTTAGTAGAGAGGGGTTTACCATGTTGGCCAGGCTGGTATCAAC 3600  
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DB CTTTCACCTTCCAAGTCAGGTAGGTAGTTCAATCTAGTTGTTAGGCCAAGGACTCAAGGACTG 3960  
QY 3961 AATTGTTTTTAAACATAAGCTTTTCTGTTCTGGAGCGGCACTTCATTTAAATTTCTCTA 4020  
DB AATTGTTTTTAAACATAAGCTTTTCTGTTCTGGAGCGGCACTTCATTTAAATTTCTCTA 4020  
QY 4021 AAACCTGTATGTTTAGAGTTAAAGCAAGACTTTTTTCTCTCTCCATGAGTTGTAAT 4080  
DB AAACCTGTATGTTTAGAGTTAAAGCAAGACTTTTTTCTCTCTCCATGAGTTGTAAT 4080  
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QY 4201 ACAGCATTTGCTGTTGTTGAACATATAAAAAAGCAGCGGATCTTTTCCATCTAATTTCCGCA 4260





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Db 841 TTTACTTTTGGGACATGATATACTCAGTTAAACAAGGAGCAGCTTCAAGAGAGCTGGATTT 900  
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Db 1081 GAGTGTCTGTGAAGTACTTGAAGAAACACCATCACTAACTAGAGAAATTTGATGATACC 1140  
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QY TTCAAGCAAAAAATTTTATGCTTAACTTAATCTAAGTCTATAGTAGGCATGTTATCTTCT 1560  
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QY TAGCATTTGCTACCAAGTAGGAAAAAATGATACATGCGCAGTGTGTTAGTGGCAATATA 1680  
Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGATACATGCGCAGTGTGTTAGTGGCAATATA 1680  
QY ACTTTTGAATTTCTGATTTTTCAGGGTATAGCTGATATATCCATTTTTTACTGTTA 1740  
Db 1681 ACTTTTGAATTTCTGATTTTTCAGGGTATAGCTGATATATCCATTTTTTACTGTTA 1740  
QY TTTAAATGAACCATAGACTAAGAAATGAAGCATCATACTATAACTGAACACAAATGTGT 1800  
Db 1741 TTTAAATGAACCATAGACTAAGAAATGAAGCATCATACTATAACTGAACACAAATGTGT 1800  
QY ATTCATAGTATCTGATTTAAATTTCTAAGTGTAAAGTGAATTAATCATCTCGATTTTTAT 1860  
Db ATTCATAGTATCTGATTTAAATTTCTAAGTGTAAAGTGAATTAATCATCTCGATTTTTAT

Db 1801 ATTCATAGTATCTGATTTAAATTTCTAAGTGTAAAGTGAATTAATCATCTCGATTTTTAT 1860  
QY TCCTTTTCAGATAGGCTTACAAATGAGGCTTCTCTGATATATAAAATGTTGAGATAGAGTTA 1920  
Db 1861 TCCTTTTCAGATAGGCTTACAAATGAGGCTTCTCTGATATATAAAATGTTGAGATAGAGTTA 1920  
QY ATCTCCCAATCACATAAATTTGTTGTGTGAAAAAGGAATAAATTTGTTCCATCTGCTGGT 1980  
Db 1921 ATCTCCCAATCACATAAATTTGTTGTGTGAAAAAGGAATAAATTTGTTCCATCTGCTGGT 1980  
QY GAAAGATAGAGATTTGTTTAGAGGTTGGTGTGTTTAGAGATTTCTCTCAGATTTCT 2040  
Db 1981 GAAAGATAGAGATTTGTTTAGAGGTTGGTGTGTTTAGAGATTTCTCTCAGATTTCT 2040  
QY TTTAAAGTTATAAACAAGTACTTGTGCGAATTAATTTTTTAAAGTGAATTTGCCATTTTG 2100  
Db 2041 TTTAAAGTTATAAACAAGTACTTGTGCGAATTAATTTTTTAAAGTGAATTTGCCATTTTG 2100  
QY AAAGCGTATTTAATGATAGAAATCTATCGAGCCAAACATGTACTGACATGGAAGATGCTA 2160  
Db 2101 AAAGCGTATTTAATGATAGAAATCTATCGAGCCAAACATGTACTGACATGGAAGATGCTA 2160  
QY AAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATATATAGTCTGAGCCAGATCA 2220  
Db 2161 AAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATATATAGTCTGAGCCAGATCA 2220  
QY AAGTATGTTAAGTGTAAATGCAAGTGGCAAAACACTATATATAGTCTGAGCCAGATCA 2220  
Db 2221 AAGTATGTTAAGTGTAAATGCAAGTGGCAAAACACTATATATAGTCTGAGCCAGATCA 2220  
QY TTAAGTGTGGTTCTCTCGGGAGGGGGGATTGGGGAGGGGGCCCGAGAGGGGTTTA 2340  
Db 2281 TTAAGTGTGGTTCTCTCGGGAGGGGGGATTGGGGAGGGGGCCCGAGAGGGGTTTA 2340  
QY TAGGGGCTTTTTCACCTTTCTACCTTTTTCATTTTGTCTGCTGCAATTTTATTAAGTAT 2400  
Db 2341 TAGGGGCTTTTTCACCTTTTCTACCTTTTTCATTTTGTCTGCTGCAATTTTATTAAGTAT 2400  
QY GTATTACTTTTGTAAATCAGAAATTTTAGAAGTATTTTGTCTGATTTAAAGCTTTAGGCA 2460  
Db 2401 GTATTACTTTTGTAAATCAGAAATTTTAGAAGTATTTTGTCTGATTTAAAGCTTTAGGCA 2460  
QY GTTCAACCGCTGCAAAACCTATTACCTCAGCTTTAGTCTTTTCTAATCAAGAGGCA 2520  
Db 2461 GTTCAACCGCTGCAAAACCTATTACCTCAGCTTTAGTCTTTTCTAATCAAGAGGCA 2520  
QY GGCAGTTAACTTTTGTGGCCAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 2580  
Db 2521 GGCAGTTAACTTTTGTGGCCAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 2580  
QY TGTGGATGAAAAATATTTCTGAGTGGTGTGTTTGTGACAGGTAGACCATGCTTATCTTG 2640  
Db 2581 TGTGGATGAAAAATATTTCTGAGTGGTGTGTTTGTGACAGGTAGACCATGCTTATCTTG 2640  
QY TTTCAAAATAAGTATTTCTGATTTTGTAAATGAAATATAAATATGCTCAGATCTTCC 2700  
Db 2641 TTTCAAAATAAGTATTTCTGATTTTGTAAATGAAATATAAATATGCTCAGATCTTCC 2700  
QY AATTAATAGTAGGATTCATCTTAATCTGCTAGTTTAAAGCTGCTTAAAGTCACTTT 2760  
Db 2701 AATTAATAGTAGGATTCATCTTAATCTGCTAGTTTAAAGCTGCTTAAAGTCACTTT 2760  
QY ACTAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGAGTAAAGT 2820  
Db 2761 ACTAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGAGTAAAGT 2820  
QY AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTTCCATGTTGAGATTTCTCA 2880  
Db 2821 AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTTCCATGTTGAGATTTCTCA 2880  
QY TATCATCTTGTATCTTAAAGTTTTCATGTGAGTTTACCCTTAGGATGATTAAGATGAT 2940  
Db TATCATCTTGTATCTTAAAGTTTTCATGTGAGTTTACCCTTAGGATGATTAAGATGAT

Qy	2941	ATAGGACAAAATGTTAAGTCTTCTCTACCTACATTTGTTTTCTTGCTAGTAATAAGTA	3000
Db	2941	ATAGGACAAAATGTTAAGTCTTCTCTACCTACATTTGTTTTCTTGCTAGTAATAAGTA	3000
Qy	3001	GTAGATACTTCTGAAATAAATGTTCTCTCAAGATCCCTTAAACCTCTTGGAAATATATAA	3060
Db	3001	GTAGATACTTCTGAAATAAATGTTCTCTCAAGATCCCTTAAACCTCTTGGAAATATATAA	3060
Qy	3061	AATATTGGCAAGAAAAGAAATAGTTGTTTAAATATATTTTTTAAAAACACTTCAATAAG	3120
Db	3061	AATATTGGCAAGAAAAGAAATAGTTGTTTAAATATATTTTTTAAAAACACTTCAATAAG	3120
Qy	3121	AATCAGTAGGGTATAAAGTATAGAGTTTAAAAATGCTCATAGAACGTCACAGGTTTACAT	3180
Db	3121	AATCAGTAGGGTATAAAGTATAGAGTTTAAAAATGCTCATAGAACGTCACAGGTTTACAT	3180
Qy	3181	TACAAGATTCTCACACAAACCCATTGTAGAGGTGAGTAAAGCATGTTTACTACAGAGAA	3240
Db	3181	TACAAGATTCTCACACAAACCCATTGTAGAGGTGAGTAAAGCATGTTTACTACAGAGGAA	3240
Qy	3241	AGTTTGAGAGTAAACCTGTAATAAATATATTTTTTGTGTACTTCTTAAGAGAAAGAGTA	3300
Db	3241	AGTTTGAGAGTAAACCTGTAATAAATATATTTTTTGTGTACTTCTTAAGAGAAAGAGTA	3300
Qy	3301	TGTTATGTTCTCCTAACTTCTGTGTATTACTACATTTAAGTGAATATCATTTAAAAACATT	3360
Db	3301	TGTTATGTTCTCCTAACTTCTGTGTATTACTACATTTAAGTGAATATCATTTAAAAACATT	3360
Qy	3361	GCAAAATTTATTTTATTTTAAATTTCTCTTTTGAGATGGAGTCTGCTGTCTCACCCAGG	3420
Db	3361	GCAAAATTTATTTTATTTTAAATTTCTCTTTTGAGATGGAGTCTGCTGTCTCACCCAGG	3420
Qy	3421	CTGGAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCTCTTGGGTTCAAGCGAT	3480
Db	3421	CTGGAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCTCTTGGGTTCAAGCGAT	3480
Qy	3481	TCCTGCTCCTCAGCTTCCTGAGTAGTGGATTTACAGGAGGTGGCACCATTGCCCGACTA	3540
Db	3481	TCCTGCTCCTCAGCTTCCTGAGTAGTGGATTTACAGGAGGTGGCACCATTGCCCGACTA	3540
Qy	3541	ATTTTTTTTTTATTTTTAGTAGACGGGTTTCACCATGTTGGCCAGGCTGGTATCAAC	3600
Db	3541	ATTTTTTTTTTATTTTTAGTAGACGGGTTTCACCATGTTGGCCAGGCTGGTATCAAC	3600
Qy	3601	TCCTGACCTCAAGAGATCCACTCGCTTCGCCCTCCCAAGTCTGGGATACAGGCTTGA	3660
Db	3601	TCCTGACCTCAAGAGATCCACTCGCTTCGCCCTCCCAAGTCTGGGATACAGGCTTGA	3660
Qy	3661	GCCACACGCCCGGCTTAAACATTCGAATTTAAATGAGAGTTTTTAAAAATTAATAATG	3720
Db	3661	GCCACACGCCCGGCTTAAACATTCGAATTTAAATGAGAGTTTTTAAAAATTAATAATG	3720
Qy	3721	ACTGCCCTGTTCTGTTTTAGTAGTATGTAATCTCAGTCTTCACCTTGCACTGCTGCC	3780
Db	3721	ACTGCCCTGTTCTGTTTTAGTAGTATGTAATCTCAGTCTTCACCTTGCACTGCTGCC	3780
Qy	3781	ACTTAGTTTTGGTTATATAGTCAATTAACTGAAATTTGGTCTGTATAGTCTAGACTTTAAAT	3840
Db	3781	ACTTAGTTTTGGTTATATAGTCAATTAACTGAAATTTGGTCTGTATAGTCTAGACTTTAAAT	3840
Qy	3841	TTAAAGTTTTCTACAAGGGGAGAAAGTGTAAAAATTTTTTAAAAATATGTTTTCCAGGACA	3900
Db	3841	TTAAAGTTTTCTACAAGGGGAGAAAGTGTAAAAATTTTTTAAAAATATGTTTTCCAGGACA	3900
Qy	3901	CTTCACCTTCCAAGTCAAGTAGGTAGTTCAATCTAGTCTGTAGCCAAAGGACTCAAGGACTG	3960
Db	3901	CTTCACCTTCCAAGTCAAGTAGGTAGTTCAATCTAGTCTGTAGCCAAAGGACTCAAGGACTG	3960
Qy	3961	AATGTTTTTAAACATAAGGCTTTTCCGTGCTGGGAGCGGCACTTCATTAATAATTTCTCTA	4020
Db	3961	AATGTTTTTAAACATAAGGCTTTTCCGTGCTGGGAGCGGCACTTCATTAATAATTTCTCTA	4020

QY	4021	AAACTGTGATGTTT	TAGAGTTAAGCAAGACTTT	TTTTTCTTCCCTCCATGAGTTGTGAAT	4080	
DB	4021	AAACTGTGATGTTT	TAGAGTTAAGCAAGACTTT	TTTTTCTTCCCTCCATGAGTTGTGAAT	4080	
QY	4081	TTAATGCACAACGC	TCGATCGTGGCTAACAAAGTTAT	TTTTTAAAGAAATGTTT	TAGAATGCTGT	4140
DB	4081	TTAATGCACAACGC	TCGATCGTGGCTAACAAAGTTAT	TTTTTAAAGAAATGTTT	TAGAATGCTGT	4140
QY	4141	TGCTTCAGGTTCTT	AAAAATCACTCAGCACTCCAACTTC	TAAATCAAAATTTTTT	TGGAGACTTA	4200
DB	4141	TGCTTCAGGTTCTT	AAAAATCACTCAGCACTCCAACTTC	TAAATCAAAATTTTTT	TGGAGACTTA	4200
QY	4201	ACAGCAATTTGTC	TGTTGAACTATAAAAGCACCGGATCT	TTTCCATCTAATTTCCGCA	4260	
DB	4201	ACAGCAATTTGTC	TGTTGAACTATAAAAGCACCGGATCT	TTTCCATCTAATTTCCGCA	4260	
QY	4261	AAAAATGATCATTT	TGCAAAAGTCAAAACTATAGCCATAT	CCAAATCTTTTCCCCCTCCCA	4320	
DB	4261	AAAAATGATCATTT	TGCAAAAGTCAAAACTATAGCCATAT	CCAAATCTTTTCCCCCTCCCA	4320	
QY	4321	GAGTTCTCAGTGCT	ACATGCTAGACATATTCCTTTTCTG	TATAAGTTTCACTCTAGGATTT	4380	
DB	4321	GAGTTCTCAGTGCT	ACATGCTAGACATATTCCTTTTCTG	TATAAGTTTCACTCTAGGATTT	4380	
QY	4381	CAAGTCACCACCT	TATTTTACATTTTAGTCATGCAAAAGATT	CAAGTAGTTTTCGCAATAAGT	4440	
DB	4381	CAAGTCACCACCT	TATTTTACATTTTAGTCATGCAAAAGATT	CAAGTAGTTTTCGCAATAAGT	4440	
QY	4441	ACTTATCTTTATTT	TGTAATAATTAGTCGCTGATCAAAAGCAAT	TGCTTTAAATTTTGTAG	4500	
DB	4441	ACTTATCTTTATTT	TGTAATAATTAGTCGCTGATCAAAAGCAAT	TGCTTTAAATTTTGTAG	4500	
QY	4501	AACTGGTTTTAGCAT	TTACAAACTAAATTCAGTTAAATTAATTA	TAATAGCTTTATATTGCC	4560	
DB	4501	AACTGGTTTTAGCAT	TTACAAACTAAATTCAGTTAAATTAATTA	TAATAGCTTTATATTGCC	4560	
QY	4561	TTTCTGCTACAT	TTTGGTTTTTCCCTTGCTCCCTTTGATT	ACGGCTAAGGTAGGTAAG	4620	
DB	4561	TTTCTGCTACAT	TTTGGTTTTTCCCTTGCTCCCTTTGATT	ACGGCTAAGGTAGGTAAG	4620	
QY	4621	ANNGGTGTAGTGAG	TGTATATAATGTGATTTGGCCCTGTGTAAT	TATGATATTTTGTAT	4680	
DB	4621	ANNGGTGTAGTGAG	TGTATATAATGTGATTTGGCCCTGTGTAAT	TATGATATTTTGTAT	4680	
QY	4681	TTTTTGTGTTATAT	TATTTACATTTCCAGTAGTTGTTTTTGTG	CTTCCATTTTAGGGGAT	4740	
DB	4681	TTTTTGTGTTATAT	TATTTACATTTCCAGTAGTTGTTTTTGTG	CTTCCATTTTAGGGGAT	4740	
QY	4741	AAAAATTTGATTT	TGAACATGAATGGAGACTACCGCCCGCAGCAT	TAGTTTTCACATGATA	4800	
DB	4741	AAAAATTTGATTT	TGAACATGAATGGAGACTACCGCCCGCAGCAT	TAGTTTTCACATGATA	4800	
QY	4801	TACCCCTTTAAAC	CCGAATCATTTGTTTTTATTTCTGAT	TACACAGGTGTTGAAATGGGGAAA	4860	
DB	4801	TACCCCTTTAAAC	CCGAATCATTTGTTTTTATTTCTGAT	TACACAGGTGTTGAAATGGGGAAA	4860	
QY	4861	GGGGCTAGTATAT	ATCAGTAGGATATCTATGGGATGTATATATAT	CAATCTGTTTAGAGAA	4920	
DB	4861	GGGGCTAGTATAT	ATCAGTAGGATATCTATGGGATGTATATATAT	CAATCTGTTTAGAGAA	4920	
QY	4921	ATGAATAAAAT	GGGGCTGGGCTCAGTGGGTACGGCTGTAAAT	CCCGAGCACTTTGGGAGG	4980	
DB	4921	ATGAATAAAAT	GGGGCTGGGCTCAGTGGGTACGGCTGTAAAT	CCCGAGCACTTTGGGAGG	4980	
QY	4981	CTGAGGCAGGTGAT	CAACAGGTTCAGAGATTCGAGACCATCT	CTGGCTTAACACCGGTGAAC	5040	
DB	4981	CTGAGGCAGGTGAT	CAACAGGTTCAGAGATTCGAGACCATCT	CTGGCTTAACACCGGTGAAC	5040	
QY	5041	CCCGTCTCTACT	TAATAAAACAGAAAAATAGCCGGCGTGT	GGCGGCGCTGTAGTCCCA	5100	
DB	5041	CCCGTCTCTACT	TAATAAAACAGAAAAATAGCCGGCGTGT	GGCGGCGCTGTAGTCCCA	5100	
QY	5101	GCTACTCGGAGGCT	CTGAGGCAGGAGAAATGGTGTGAACCCCGGAGG	CAAGACTTGCAGTGA	5160	



Db 88110 CCAATAGACTAAGAAATGAAAGCATCATACTATAACTGAACCAATGTGTATATTCATAGTAT 88051  
Qy 1812 ACTGATTTAAATTTCTAAGTGTAAGTGAATTAATCATCTGGGATTTTATTTATCTTTTCAGAT 1871  
Db 88050 ACTGATTTAAATTTCTAAGTGTAAGTGAATTAATCATCTGGGATTTTATTTATCTTTTCAGAT 87991  
Qy 1872 AGGCTTAACAAATGGAGCTTTCTGTATATAAAATGFGAGATTTAGAGTTAAATCTCCCCAAT 1931  
Db 87990 AGGCTTAACAAATGGAGCTTTCTGTATATAAAATGFGAGATTTAGAGTTAAATCTCCCCAAT 87931  
Qy 1932 CACATAATTTGTTTCTGTGTAAGAAAGGAATAAATGTTCCATGCTGTGGGAAAGATAGAG 1991  
Db 87930 CACATAATTTGTTTCTGTGTAAGAAAGGAATAAATGTTCCATGCTGTGGGAAAGATAGAG 87871  
Qy 1992 ATTTGTTTATAGAGTTGGTGTGTGTTTATAGGATTTCTGTCATTTCTTTTAAAGTTAT 2051  
Db 87870 ATTTGTTTATAGAGTTGGTGTGTGTTTATAGGATTTCTGTCATTTCTTTTAAAGTTAT 87811  
Qy 2052 AAACACGTACTGTGCGAATTAATTTTAAAGTGATTTGCCATTTTGAAGCGTATTT 2111  
Db 87810 AAACACGTACTGTGCGAATTAATTTTAAAGTGATTTGCCATTTTGAAGCGTATTT 87751  
Qy 2112 AATGATAGAACTACTGAGGCCAATGCTACTGACATGGAAGATGTCAAAGATATGTTA 2171  
Db 87750 AATGATAGAACTACTGAGGCCAATGCTACTGACATGGAAGATGTCAAAGATATGTTA 87691  
Qy 2172 AGTGTAAATGCAAGTGGCAAAACACTATGATAGTCTGAGCCAGATCAAAAGTATGATG 2231  
Db 87690 AGTGTAAATGCAAGTGGCAAAACACTATGATAGTCTGAGCCAGATCAAAAGTATGATG 87631  
Qy 2232 TTTTAAATGATAGTAAACAAAGATTTGGAAGATATACACCAACTGTTTAAATGTGGT 2291  
Db 87630 TTTTAAATGATAGTAAACAAAGATTTGGAAGATATACACCAACTGTTTAAATGTGGT 87571  
Qy 2292 TTCTCTCGGGAGGGGGATTTGGGGAGGGGCCCCAGAGGGGTTTATAGGGCCCTTT 2351  
Db 87570 TTCTCTCGGGAGGGGGATTTGGGGAGGGGCCCCAGAGGGGTTTATAGGGCCCTTT 87511  
Qy 2352 TCACCTTTCTACTTTTTCATTTTGTCTGTTCTGTAATTTTATAGTATGATTTACTTTT 2411  
Db 87510 TCACCTTTCTACTTTTTCATTTTGTCTGTTCTGTAATTTTATAGTATGATTTACTTTT 87451  
Qy 2412 GTAATCAGAAATTTTAGAAATTTTCTGATTTTAAAGGCTTAGGCAATGTTCAACGCC 2471  
Db 87450 GTAATCAGAAATTTTAGAAATTTTCTGATTTTAAAGGCTTAGGCAATGTTCAACGCC 87391  
Qy 2472 TGCAAACTACTTATCACTCAGCTTTAGTGTCTTAATCCAAAGGAGGAGGCAAGTTAAC 2531  
Db 87390 TGCAAACTACTTATCACTCAGCTTTAGTGTCTTAATCCAAAGGAGGAGGCAAGTTAAC 87331  
Qy 2532 CTTTTTGTGCCAATGTGAAATGTAATGATTTTATGTTTCTGCTTTTCTGATGAA 2591  
Db 87330 CTTTTTGTGCCAATGTGAAATGTAATGATTTTATGTTTCTGCTTTTCTGATGAA 87271  
Qy 2592 AATATTTCTGAGTGGTATTTTTCAGAGGTAGACCATGCTTATCTGTTTCAAAATAA 2651  
Db 87270 AATATTTCTGAGTGGTATTTTTCAGAGGTAGACCATGCTTATCTGTTTCAAAATAA 87211  
Qy 2652 GTATTTCTGATTTTCTAAATGAATATAAATATGTCATGCTCAGATCTTCCAATTAATAGT 2711  
Db 87210 GTATTTCTGATTTTCTAAATGAATATAAATATGTCATGCTCAGATCTTCCAATTAATAGT 87151  
Qy 2712 AAGGATTCATCTTAATCTTGTAGTTTAAAGCTGCTTAAGTCACTTTACTTAAAGATC 2771  
Db 87150 AAGGATTCATCTTAATCTTGTAGTTTAAAGCTGCTTAAGTCACTTTACTTAAAGATC 87091  
Qy 2772 TTTGTTAACTCAGTATTTTAAACATCTGTACAGCTTATGTAGGTAAGTAAAGTACATGTT 2831  
Db 87090 TTTGTTAACTCAGTATTTTAAACATCTGTACAGCTTATGTAGGTAAGTAAAGTACATGTT 87031  
Qy 2832 TGTACACTGCTGTAGTATATAGTACACACTTTCCATGTTTGAGATTTCTCATATCATCTGT 2891  
Db 87031 TGTACACTGCTGTAGTATATAGTACACACTTTCCATGTTTGAGATTTCTCATATCATCTGT

Db 87030 TGTACACTGCTGTAGTATATAGTACACACTTTCCATGTTTGAGATTTCTCATATCATCTGT 86971  
Qy 2892 ATCTTAAAGTTTTCATGTGAGTGTATTTACCGTTAGGATGATTAAGATGTATATAGACAAA 2951  
Db 86970 ATCTTAAAGTTTTCATGTGAGTGTATTTACCGTTAGGATGATTAAGATGTATATAGACAAA 86911  
Qy 2952 TGTAAAGTCTTCTCTACCTACCTACATTTGTTTCTGTTGGCTAGTAATAGTAGTACATCTC 3011  
Db 86910 TGTAAAGTCTTCTCTACCTACCTACATTTGTTTCTGTTGGCTAGTAATAGTAGTACATCTC 86851  
Qy 3012 TGAATTAATCTTCTCTCAAGATCCTTAAACCTCTTGGAAATTTATAAAATATTTGGCAA 3071  
Db 86850 TGAATTAATCTTCTCTCAAGATCCTTAAACCTCTTGGAAATTTATAAAATATTTGGCAA 86791  
Qy 3072 GAAAGAAAGATAGTGTGTTTAAATATTTTAAACACCTTGAATAAGAACTCAGTAGGG 3131  
Db 86790 GAAAGAAAGATAGTGTGTTTAAATATTTTAAACACCTTGAATAAGAACTCAGTAGGG 86731  
Qy 3132 TATAAAGTGTGTTTAAATGCTCATAGAACTCCAGGGTTTACATTTACAAGATTTCT 3191  
Db 86730 TATAAAGTGTGTTTAAATGCTCATAGAACTCCAGGGTTTACATTTACAAGATTTCT 86671  
Qy 3192 CACAACAAACCTATGTAGAGGTGAGTAAGCATGTTTACTACAGAGGAAAGTGTGAGAGT 3251  
Db 86670 CACAACAAACCTATGTAGAGGTGAGTAAGCATGTTTACTACAGAGGAAAGTGTGAGAGT 86611  
Qy 3252 AAAAAGTGTGTTTAAATATTTTGTGTTTCTTAAGAGAAAGATTTGTTATGTTTC 3311  
Db 86610 AAAAAGTGTGTTTAAATATTTTGTGTTTCTTAAGAGAAAGATTTGTTATGTTTC 86551  
Qy 3312 TCCTAACTCTGTTGATTTACTTAAAGTGTATTTCAATTTAAACATTTGCAATTTTAT 3371  
Db 86550 TCCTAACTCTGTTGATTTACTTAAAGTGTATTTCAATTTAAACATTTGCAATTTTAT 86491  
Qy 3372 TTAATTTTAAATTTCTTTTGTAGAGTGAGTCTGTTGTCACCCAGGCTGGAGTGAG 3431  
Db 86490 TTAATTTTAAATTTCTTTTGTAGAGTGAGTCTGTTGTCACCCAGGCTGGAGTGAG 86431  
Qy 3432 TGGAGTGTATCTGCTCAGTCAACCTCCGCTTCTGTTGTTCAAGCGATTTCTGTCGCTC 3491  
Db 86430 TGGAGTGTATCTGCTCAGTCAACCTCCGCTTCTGTTGTTCAAGCGATTTCTGTCGCTC 86371  
Qy 3492 AGCTTCTGAGTGTGGAATTTACAGGAGGTGGCACCACCTGATTTTCTTTT 3551  
Db 86370 AGCTTCTGAGTGTGGAATTTACAGGAGGTGGCACCACCTGATTTTCTTTT 86311  
Qy 3552 TTTTGTAGTAGAGCGGGTTTTCACCATGTTGGCAGGCTGGTATCAAACTCCTGACCTCA 3611  
Db 86310 TTTTGTAGTAGAGCGGGTTTTCACCATGTTGGCAGGCTGGTATCAAACTCCTGACCTCA 86251  
Qy 3612 AGAGATCCACTCGCTTCCCTCCCAAGTGTGGATTTACAGGCTTGAGCCACACGCC 3671  
Db 86250 AGAGATCCACTCGCTTCCCTCCCAAGTGTGGATTTACAGGCTTGAGCCACACGCC 86191  
Qy 3672 CGGCTAAACATTTGCAATTTTAAATGAGATTTTAAATTAATATGACCTGCTGTT 3731  
Db 86190 CGGCTAAACATTTGCAATTTTAAATGAGATTTTAAATTAATATGACCTGCTGTT 86131  
Qy 3732 TCTGTTTGTAGTATGTAATCTCAGTCTTCCACCTTTCACCTGCTGCTGCTGCTGCTGCT 3791  
Db 86130 TCTGTTTGTAGTATGTAATCTCAGTCTTCCACCTTTCACCTGCTGCTGCTGCTGCTGCT 86071  
Qy 3792 TTATATAGTCTTAACTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTTC 3851  
Db 86070 TTATATAGTCTTAACTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTTC 86011  
Qy 3852 TACAAGGGGAGAAAGTGTAAAAATTTTAAAAATATGTTTTCAGGACACTTCACTTCCA 3911  
Db 86010 TACAAGGGGAGAAAGTGTAAAAATTTTAAAAATATGTTTTCAGGACACTTCACTTCCA 85951  
Qy 3912 AGTCAGGTAGTGTCAATCTAGTGTGTACCCAGGACTCAAGGACTGAATTTGTTTAA 3971  
Db 85950 AGTCAGGTAGTGTCAATCTAGTGTGTACCCAGGACTCAAGGACTGAATTTGTTTAA 85891

QY 3972 CATAAGGCTTTTCTGTTCTGGAGCGGCACCTTCATTAAAAATTTCTTAAAACTTGTATG 4031  
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Db 8590 CATAAGGCTTTTCTGTTCTGGAGCGGCACCTTCATTAAAAATTTCTTAAAACTTGTATG 85931  
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QY 4032 TTTAGAGTTAAGCAAGACTTTTCTTCTCCATCCATGAGTGTGAAATTTAATGACAA 4091  
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Db 85930 TTTAGAGTTAAGCAAGACTTTTCTTCTCCATCCATGAGTGTGAAATTTAATGACAA 85771  
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QY 4092 CGCTGATGTGGCTAACAGTTTATTTTAAAGATTTGTTTAAAGATGCTTGTCTCAGGTT 4151  
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Db 85770 CGCTGATGTGGCTAACAGTTTATTTTAAAGATTTGTTTAAAGATGCTTGTCTCAGGTT 85711  
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QY 4152 CTTAAAACTACTCAGCAGCTCCAACTTCTAATCAAAATTTTGGAGACTTAACAGCATTTGT 4211  
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Db 85710 CTTAAAACTACTCAGCAGCTCCAACTTCTAATCAAAATTTTGGAGACTTAACAGCATTTGT 85651  
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QY 4212 CTGCTGTTGAACATAAAAAAGCAGCGGATCTTTTCCATCAATTAATTCGCCAAAAATTTGATCA 4271  
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Db 85650 CTGCTGTTGAACATAAAAAAGCAGCGGATCTTTTCCATCAATTAATTCGCCAAAAATTTGATCA 85591  
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QY 4272 TTTGCAAGTCAAAACATATAGCCATATCCAAATCTTTTCCCTCCCAAGATTTCTCAGT 4331  
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Db 85590 TTTGCAAGTCAAAACATATAGCCATATCCAAATCTTTTCCCTCCCAAGATTTCTCAGT 85531  
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QY 4332 GTCTACATGTAGACTATTCTCTCTGTATAAAGTTTCACTCTAGGATTTCAAGTCACCAC 4391  
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Db 85530 GTCTACATGTAGACTATTCTCTCTGTATAAAGTTTCACTCTAGGATTTCAAGTCACCAC 85471  
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QY 4392 TTAATTTACATTTTAGTCATGCAAGATTTCAAGTAGTTTTCGCAATAAGTACTTATCTTTA 4451  
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Db 85470 TTAATTTACATTTTAGTCATGCAAGATTTCAAGTAGTTTTCGCAATAAGTACTTATCTTTA 85411  
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QY 4452 TTTGTAATAATTAGTCTGTGATCAAAAGCATTTCTTAATTTTTCGAGAACTGGTTTAA 4511  
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Db 85410 TTTGTAATAATTAGTCTGTGATCAAAAGCATTTCTTAATTTTTCGAGAACTGGTTTAA 85351  
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QY 4512 GCATTTACAAACTAAATTCAGTTTAAATTAATAGCTTATATTCCTTTCTCTGCTAC 4571  
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Db 85350 GCATTTACAAACTAAATTCAGTTTAAATTAATAGCTTATATTCCTTTCTCTGCTAC 85291  
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QY 4572 ATTTGGTTTTTCCCTGTCCTTTGATACGGGCTAAGGTAGGTTAAGANNGGTTAG 4631  
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Db 85290 ATTTGGTTTTTCCCTGTCCTTTGATACGGGCTAAGGTAGGTTAAGANNGGTTAG 85232  
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QY 4632 TGAGTGATATATGATGATTTGGCCCTGTGATATATATATTTTGTATTTTCTTTCTTA 4691  
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DEFINITION  
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Contains a PDZ (DHR, GLGF) domain protein pseudogene, the AP13 gene  
for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene,  
ESTs, STSs, GSSs and a putative CpG island, complete sequence.  
AL121601  
ACCESSION  
AL121601.13 GI:7159760  
VERSION  
HTG; AP13; CpG island; DHR; GLGF; HILP; PDZ; XIAP.  
KEYWORDS  
SOURCE  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 133391)  
Direct Submission  
Grapham.D.  
REFERENCE  
Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,  
Ch10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
JOURNAL  
requests: clonerequest@sanger.ac.uk  
COMMENT  
On Mar 6, 2000 this sequence version replaced gi:6983378.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated human repeat sequence elements (e.g. Alu). Where the  
sequence is ambiguous, there is an annotation using the 'unsure'  
feature key.  
The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information  
on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C-elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome X, constructed by the Sanger Centre Chromosome X Mapping  
Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/ChrX  
RP1-315G1 is from the library RP1-1 constructed at the Roswell  
Park Cancer Institute by the group of Pieter de Jong. For further  
details see http://bacpac.med.buffalo.edu/  
VECTOR: pCYPAC2  
This sequence is the entire insert of clone RP1-315G1 The true  
right end of clone RP6-30A23 is at 100 in this sequence.  
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LOCUS	HS424J12/c		
DEFINITION	Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCING IN	201197 bp	DNA linear HTG 10-JUL-2001
ACCESSION	PROGRESS ***, 15 unordered pieces.		
VERSION	282207.3	GI:123331276	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_CANCELLED.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 201197)		
JOURNAL	Direct Submission		
	Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,		
	CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk		
	requests: clonerquest@sanger.ac.uk		
	On Jan 22, 2001 this sequence version replaced gi:10045116.		
COMMENT	----- Genome Center		
	Center: Sanger Centre		
	Center code: SC		
	Web site: http://www.sanger.ac.uk		
	Contact: humquery@sanger.ac.uk		
	----- Project Information		
	Center project name: dJ424J12		
	----- Summary Statistics		
	Assembly program: XGAP4; version 4.5		
	Sequencing vector: M13; M7815; 74% of reads		
	Sequencing vector: plasmid; L08752; 25% of reads		



Chemistry: Dye-terminator Big Dye; 0% of reads  
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 Insert size: 199797; sum-of-contigs  
 Quality coverage: 6.87x in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 15 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 4154: contig of 4154 bp in length  
 \* 4155 4254: gap of 100 bp  
 \* 4255 18703: contig of 14449 bp in length  
 \* 18704 18803: gap of 100 bp  
 \* 18804 20941: contig of 2138 bp in length  
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 \* 34908 35012: gap of 105 bp  
 \* 35013 37508: contig of 2496 bp in length  
 \* 37509 37608: gap of 100 bp  
 \* 37609 52739: contig of 15131 bp in length  
 \* 52740 52839: gap of 100 bp  
 \* 52840 56933: contig of 4094 bp in length  
 \* 56934 57033: gap of 100 bp  
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 \* 88246 88346: gap of 101 bp  
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 \* 93387 93486: gap of 100 bp  
 \* 93487 123956: contig of 30470 bp in length  
 \* 123957 124056: gap of 100 bp  
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## FEATURES

source

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LOCUS AX412131 3000 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 231 from Patent WO0226968.  
ACCESSION AX412131  
VERSION AX412131.1 GI:21444588  
KEYWORDS

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
  
REFERENCE 1  
AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
TITLE Antisense iap nucleic acids and uses thereof  
JOURNAL Patent: WO 0226968-A 231 04-APR-2002;  
University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)  
  
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REFERENCE	Authors		
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TITLE	Transgenic drosophila melanogaster expressing beta amyloid		
JOURNAL	Patent: WO 0226820-A 38 04-APR-2002;		
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LOCUS

AR103281 2540 bp DNA linear PAT 14-FEB-2001

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ACCESSION ARI03281  
VERSION ARI03281.1 GI:12814869  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2540)  
AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowser,L.M.  
TITLE Antisense modulation of x-linked inhibitor of apoptosis expression  
JOURNAL Patent: US 6087173-A 1 11-JUL-2000;  
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BASE COUNT 781 a 415 c 571 g 773 t  
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LOCUS Sequence 218 from Patent W00226968.  
DEFINITION AX412118  
ACCESSION AX412118  
VERSION AX412118.1 GI:21444581  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
AUTHORS Antisense iap nucleic acids and uses thereof  
TITLE Patent: WO 0226968-A 218 04-APR-2002;  
JOURNAL University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)  
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Best Local Similarity 100.0%; Pred. No. 0;  
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RESULT 10
LOCUS HSD45880 2540 bp mRNA linear PRI 16-FEB-1996
DEFINITION Human X-linked inhibitor of apoptosis protein XIAP mRNA, complete cds.
ACCESSION U45880.1 GI:1184319
VERSION 1
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
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AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Liston, P., Roy, N., Tamai, K., Lefebvre, C., Baird, S., Cherton-Horvat, G., Farahani, R., McLean, M., Ikeda, J., MacKenzie, A., and Korneluk, R.G.
Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes
JOURNAL Nature 379 (6563), 349-353 (1996)
MEDLINE 96149249
PUBMED 852191
REFERENCE 2 (bases 1 to 2540)
AUTHORS Baird, S.D.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-1996) Stephen D. Baird, Children's Hospital of Eastern Ontario, Genetics, 401 Smyth Rd., Ottawa, Ontario, K1H 8L1, Canada
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BC032729  
VERSION  
BC032729.1  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2086)  
Strausberg,R.  
Direct Submission  
Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)  
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
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Maduro, O.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
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Series: IRAK Plate: 69 Row: j Column: 18  
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VERSION	E31042.1	GI:13017307	
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SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 1659)		
AUTHORS	Kunihiro,M.		
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	PF 13-MAY-1998 JP 1998130378		
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DEFINITION      U32974
ACCESSION      U32974.1 GI:1016687
VERSION      apoptosis; ring finger; zinc finger.
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Duckett,C.S., Nava,V.E., Gedrich,R.W., Clem,R.J., Van Dongen,J.L.,
Gilfillan,M.C., Shiels,H., Hardwick,J.M. and Thompson,C.B.
A conserved family of cellular genes related to the baculovirus iap
gene and encoding apoptosis inhibitors
EMBO J. 15 (11), 2685-2694 (1996)
96256286
PUBMED      8654366
REFERENCE      2 (bases 1 to 1659)
Duckett,C.S. and Thompson,C.B.
Direct Submission
AUTHORS
TITLE      Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
Institute, The University of Chicago, 924 East 57th Street,
Chicago, IL 60637, USA
JOURNAL
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 201197)		
JOURNAL	Graham.D.		
COMMENT	Direct Submission		
	Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,		
	CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk		
	requests: clonerequest@sanger.ac.uk		
	On Jan 22, 2001 this sequence version replaced gi:10045116.		
	----- Genome Center		
	Center: Sanger Centre		
	Center code: SC		

Web site: <http://www.sanger.ac.uk>  
Contact: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)  
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Chemistry: Dye-terminator Big Dye; 0% of reads  
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Consensus quality: 194333 bases at least Q40  
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Insert size: 199797; sum-of-contigs  
Quality coverage: 6.87x in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 15 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
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VERSION AL390123.14 GI:16304934
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Direct Submission
Submitted (19-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clonerequest@sanger.ac.uk
On Oct 21, 2001 this sequence version replaced gi:15020926.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; SW;
SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C/elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr10
RP11-566F5 is from the library RPI1-11.2 constructed by the group
of Peter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-566F5. It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-271113 is at 156094 in this
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sequence. The true right end of clone RP11-402N18 is at 2000 in this sequence.

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2027	38.7	2404	24 AAK99405	DNA of APP related
5	1990	38.0	2540	18 AAT70836	Human apoptosis in
6	1990	38.0	2540	21 AAA64901	Human x-linked inh
7	1969	37.6	2540	24 ABK93869	Human cDNA encodin
8	1560	29.8	1659	21 AAZ48862	Human XIAP coding
9	469	9.0	469	22 AAK89469	Human digestive sy

c 10	466	8.9	489	22	ABA43584	Human breast cell
c 11	466	8.9	489	22	AAI12335	Probe #2268 for ge
c 12	466	8.9	489	22	AAI02249	Probe #2240 used t
c 13	359	6.9	417	22	AAH33140	Human colon cancer
c 14	314	6.0	315	21	AAC23231	Human secreted pro
c 15	202	3.9	1129	22	AAH99222	Human protein enco
c 16	198	3.8	1533	23	AAH74582	DNA encoding novel
c 17	198	3.8	1533	23	AAH88274	DNA encoding novel
c 18	151	2.9	190	21	AAC24217	Human secreted pro
c 19	148	2.8	148	22	ABA48694	Human breast cell
c 20	148	2.8	148	22	AAI21530	Probe #11463 for g
c 21	148	2.8	148	22	AAI07226	Probe #7217 used t
c 22	131	2.5	302	24	ABQ58785	Human colon cancer
c 23	103	2.0	40328	21	AAZ92584	Human DAZ genomic
c 24	103	2.0	43795	21	AAZ92583	Human DAZ genomic
c 25	101	1.9	160552	22	AAZ02697	Human glycosyl sul
c 26	97	1.9	7885	22	AAK70210	Human immune/haema
c 27	89	1.7	194	22	AAI36061	Human musculoskele
c 28	87	1.7	140036	24	AAH98600	Human genomic DNA
c 29	85	1.6	237	21	AAI21919	Human secreted pro
c 30	85	1.6	4274	22	AAK67096	Human immune/haema
c 31	85	1.6	5076	22	AAH16699	Human nervous syst
c 32	85	1.6	5332	22	AAH30405	DNA encoding novel
c 33	85	1.6	5332	22	AAI04432	Human reproductive
c 34	85	1.6	5372	22	AAH30406	DNA encoding novel
c 35	85	1.6	5372	22	AAI04433	Human reproductive
c 36	85	1.6	6352	22	AAH30407	DNA encoding novel
c 37	85	1.6	6352	22	AAI04434	Human reproductive
c 38	85	1.6	48203	22	AAI70161	Human immune/haema
c 39	85	1.6	48203	22	AAK81663	Human immune/haema
c 40	85	1.6	48203	22	AAK82628	Human immune/haema
c 41	85	1.6	48204	22	AAK70164	Human immune/haema
c 42	85	1.6	48204	22	AAK81666	Human immune/haema
c 43	85	1.6	48204	22	AAK82630	Human immune/haema
c 44	85	1.6	53552	22	AAH13655	Genomic DNA sequen
c 45	85	1.6	222930	24	ABK84349	Human cDNA differe

ALIGNMENTS

RESULT 1

AAV55038

ID AAV55038 standard; cDNA; 5232 bp.

XX AAV55038;

AC AAV55038;

XX 13-NOV-1998 (first entry)

DT Human XIAP coding sequence.

DE Human XIAP coding sequence.

DE Human XIAP coding sequence.

DE Human XIAP coding sequence.

DE Human XIAP coding sequence.

DE Human XIAP coding sequence.

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DE Human XIAP coding sequence.

DE Human XIAP coding sequence.

DE Human XIAP coding sequence.

XX OS Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 34..1527  
XX FT /\*tag= a  
XX FT /product= XIAP  
XX PN WO9835693-A2.  
XX PD 20-AUG-1998.  
XX PF 13-FEB-1998; 98WO-IB00781.  
XX PR 13-FEB-1997; 97US-0800929.  
XX PA (UYOT-) UNIV OTTAWA.  
XX PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;  
PI Tsang B;

XX WPI; 1998-467164/40.  
DR P-PSDB; AAW69294.  
XX  
PT Inducing apoptosis in proliferative mammalian cells with inhibitor  
PT of IAP or NAIP polypeptide - also methods for prognosis based on  
PT presence of IAP and NAIP, specifically applied to cancers involving  
PT p53 mutations  
XX  
PS Claim 13; Fig 1; 147pp; English.  
XX  
CC This sequence encodes the human XIAP protein, which is a inhibitor of  
CC apoptosis protein (IAP), and can be used in the method of the invention.  
CC The method is for enhancing apoptosis in cells from a mammal with  
CC proliferative disease by treatment with a compound that inhibits  
CC biological activity of an IAP or NAIP polypeptide. The inhibitory  
CC compounds are used to treat proliferative diseases, specially cancers of  
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,  
CC liver nasopharynx, thyroid, central nervous system, prostate, colon,  
CC rectum, cervix or endometrium, particularly to increase their sensitivity  
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are  
CC detected in many cancers and are associated with poor prognosis,  
CC resistance to chemotherapeutic agents and mutations in p53 (it is  
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP  
CC genes). Transgenic animals are used for testing the effects of antisense  
CC oligonucleotides and for screening for the inhibitors.  
XX  
SQ Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;

QY 601 TACTACACAGGTATGGTGACCAAGTCAGATGCTTTTGGTGGGAAAACTGAAAAAT 660  
DB TACTACACAGGTATGGTGACCAAGTCAGATGCTTTTGGTGGGAAAACTGAAAAAT 660  
QY 661 TGGGAACCTTGTGATCGTCTGTCAGAACACAGGCGACACTTTCCTAAATGCTCTTT 720  
DB TGGGAACCTTGTGATCGTCTGTCAGAACACAGGCGACACTTTCCTAAATGCTCTTT 720  
QY 721 GTTTTGGSCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGTCAGTCTGATAGGAAT 780  
DB GTTTTGGSCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGTCAGTCTGATAGGAAT 780  
QY 781 TTCCCAATTCACAAATCTTTCCAAAGAAATCCATCCATGGCAGATTAAGAAGCAGGATC 840  
DB TTCCCAATTCACAAATCTTTCCAAAGAAATCCATCCATGGCAGATTAAGAAGCAGGATC 840  
QY 841 TTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTTGCAGAGCTGGATTT 900  
DB TTTACTTTTGGGACATGGATATCTCAGTTAACAGGAGCAGCTTGCAGAGCTGGATTT 900  
QY 901 TATGCTTTAGTGAAGGTGATAAAGTAAAGTCTTCTACTGCGAGGAGGCTAACTCAT 960  
DB TATGCTTTAGTGAAGGTGATAAAGTAAAGTCTTCTACTGCGAGGAGGCTAACTCAT 960  
QY 961 TGSAGCCCACTGAAGACCCCTTGGGAAACACATGCTAAATGCTATCCAGGCTGCAATPAT 1020  
DB TGSAGCCCACTGAAGACCCCTTGGGAAACACATGCTAAATGCTATCCAGGCTGCAATPAT 1020  
QY 1021 CTGTTAGAACAGAGGGACAAAGATATATAACATATTCATTTAACTCATCTTCTGAG 1080  
DB CTGTTAGAACAGAGGGACAAAGATATATAACATATTCATTTAACTCATCTTCTGAG 1080  
QY 1081 GAGTGTCTGCTGTAAGAACTTACTGAGAAAACACCATCACTAAGAAATTTGATGATACC 1140  
DB GAGTGTCTGCTGTAAGAACTTACTGAGAAAACACCATCACTAAGAAATTTGATGATACC 1140  
QY 1141 ATCTTCCAAAATCCTATGTTTACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACATT 1200  
DB ATCTTCCAAAATCCTATGTTTACAAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACATT 1200  
QY 1201 AAGAAAATAATGGAGGAAAAATTCAGATATCTGGGACCACTATAAATCACTTCTGAGTT 1260  
DB AAGAAAATAATGGAGGAAAAATTCAGATATCTGGGACCACTATAAATCACTTCTGAGTT 1260  
QY 1261 CTGTTGTCAGATCTAGTGAATGCTCAGAAAACAGCTATGCAAGATGAGTCAAGTCACT 1320  
DB CTGTTGTCAGATCTAGTGAATGCTCAGAAAACAGCTATGCAAGATGAGTCAAGTCACT 1320  
QY 1321 TCATTACAGAAAGAGATTAGTACTGAGAGCAGCTAAGCGCCTGCAAGAGAGAGAGTT 1380  
DB TCATTACAGAAAGAGATTAGTACTGAGAGCAGCTAAGCGCCTGCAAGAGAGAGAGTT 1380  
QY 1381 TGCAAAATCTCTATGGATAGAAATATTCGATCGTTTTTGTTCCTTGTGGACATCTAGTC 1440  
DB TGCAAAATCTCTATGGATAGAAATATTCGATCGTTTTTGTTCCTTGTGGACATCTAGTC 1440  
QY 1441 ACTTGTAAACAAATGTGCTGAAGCAGTTGACAAAGTGTCCCATGTGCTACACAGTCACTACT 1500  
DB ACTTGTAAACAAATGTGCTGAAGCAGTTGACAAAGTGTCCCATGTGCTACACAGTCACTACT 1500  
QY 1501 TTCAAGCAAAAATTTTATCTCTTAATCTAACCTATAGTAGGAGCTGTTATGTTGTTCT 1560  
DB TTCAAGCAAAAATTTTATCTCTTAATCTAACCTATAGTAGGAGCTGTTATGTTGTTCT 1560  
QY 1561 TATTACCTGATTCGAATGCTGATGCTGAACCTGACCTTTAAGTAATCAGGATTAATTCAT 1620  
DB TATTACCTGATTCGAATGCTGATGCTGAACCTGACCTTTAAGTAATCAGGATTAATTCAT 1620  
QY 1621 TAGCATTTGCTTACCAAGTAGGAAAAAATGTACATGTCAGTGTGTTTGTGGCAATATA 1680  
DB TAGCATTTGCTTACCAAGTAGGAAAAAATGTACATGTCAGTGTGTTTGTGGCAATATA 1680  
QY 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTATTAATCCATTTTTTTTACTGTTA 1740

Db 1681 ATCTTTGAAATTTCTTGATTTTTCAGGGTATFAGCTGTATATATCATTTTCTTACTGTTA 1740  
QY TTTAAATGAAACCATAGACTAAGAAATGAAGCATCATACTATAACTGAAACAAATGCTGT 1800  
Db 1741 TTTAAATGAAACCATAGACTAAGAAATGAAGCATCATACTATAACTGAAACAAATGCTGT 1800  
QY ATTCATAGTATACTGATTTAAATTTCTAAGTGTAAGTGAATTAATCATCTCGATTTTTTAT 1860  
Db 1801 ATTCATAGTATACTGATTTAAATTTCTAAGTGTAAGTGAATTAATCATCTCGATTTTTTAT 1860  
QY TCCTTTTCAGATAGGCTTAACAAATGAGCTTCTCTGTATATAAATGTCGAGATTAGAGTTA 1920  
Db 1861 TCCTTTTCAGATAGGCTTAACAAATGAGCTTCTCTGTATATAAATGTCGAGATTAGAGTTA 1920  
QY ATCTCCCAATACATAATTTGTTGTGTGAAAAAGGAATAAATGTTCCATCTCGTGGTG 1980  
Db 1921 ATCTCCCAATACATAATTTGTTGTGTGAAAAAGGAATAAATGTTCCATCTCGTGGTG 1980  
QY 1981 GAAAGATAGAGATTGTTTTAGAGTTGGTGTGTGTTTTAGGATTCTGTCCATTTTCT 2040  
Db 1981 GAAAGATAGAGATTGTTTTAGAGTTGGTGTGTGTTTTAGGATTCTGTCCATTTTCT 2040  
QY TTTAAAGTTATAAACACGTACTTGTGCGAATTAATTTTTTAAAGTGATTTGCGCATTTTGT 2100  
Db 2041 TTTAAAGTTATAAACACGTACTTGTGCGAATTAATTTTTTAAAGTGATTTGCGCATTTTGT 2100  
QY 2101 AAAGCGTATTTAATGATAGAACTACTCGAGCCAAACATGTACTGACATGGAAGAGTCTCA 2160  
Db 2101 AAAGCGTATTTAATGATAGAACTACTCGAGCCAAACATGTACTGACATGGAAGAGTCTCA 2160  
QY 2161 AAGATATGTTAAGTGAATAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA 2220  
Db 2161 AAGATATGTTAAGTGAATAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA 2220  
QY 2221 AAGTATGATGTTTTTAATATGATAGCAACAAAGATTTGGAAGATATACACCAACTG 2280  
Db 2221 AAGTATGATGTTTTTAATATGATAGCAACAAAGATTTGGAAGATATACACCAACTG 2280  
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Db 2281 TTAATATGTTGTTCTCTCGGGGAGGGGGGATTTGGGGAGGGGCCCCAGAGGGGTTTTA 2340  
QY 2341 TAGGGCCCTTTTCACCTTTCTACCTTTTTCATTTTGTCTGCTGCAATTTTATATAAGTAT 2400  
Db 2341 TAGGGCCCTTTTCACCTTTCTACCTTTTTCATTTTGTCTGCTGCAATTTTATATAAGTAT 2400  
QY 2401 GTATTACTTTTGTAAATCAGAAATTTTGAAGAATTTTGTCTGATTTTAAAGCTTAGGCAT 2460  
Db 2401 GTATTACTTTTGTAAATCAGAAATTTTGAAGAATTTTGTCTGATTTTAAAGCTTAGGCAT 2460  
QY 2461 GTTCAACGCCCTGCAAAACCTATATACCTACCTACCTGCTTTAGTTTCTAAATCCAAAGGCA 2520  
Db 2461 GTTCAACGCCCTGCAAAACCTATATACCTACCTACCTGCTTTAGTTTCTAAATCCAAAGGCA 2520  
QY 2521 GGGCAGTTAACCTTTTGTGTGCAATGTGAAATGTAAATGATTTATGTTTTTCTGCTT 2580  
Db 2521 GGGCAGTTAACCTTTTGTGTGCAATGTGAAATGTAAATGATTTATGTTTTTCTGCTT 2580  
QY 2581 TGTGGATGAAAAATATTTCTGAGTGGTGGTTTTTGTACAGGTAGACCATGTCTTATCTTG 2640  
Db 2581 TGTGGATGAAAAATATTTCTGAGTGGTGGTTTTTGTACAGGTAGACCATGTCTTATCTTG 2640  
QY 2641 TTTCAAAATAGATTTCTGATTTTCTAATCTCTGCTAGTTTAAAGCTTAAAGCTTCTCC 2700  
Db 2641 TTTCAAAATAGATTTCTGATTTTGTAAATGAAATATAAATATATGCTTCAGATCTTCC 2700  
QY 2701 AATTAATAGTAGAGGATTCATCTTAAATCTGCTAGTTTAAAGCTTAAAGCTTAAAGCTT 2760  
Db 2701 AATTAATAGTAGAGGATTCATCTTAAATCTGCTAGTTTAAAGCTTAAAGCTTAAAGCTT 2760  
QY 2761 ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTACGCTTATGTAGTAAAGT 2820

Db 2761 ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTACGCTTATGTAGTAAAGT 2820  
QY 2821 AGAAGCATGTTTGTACACTGCTTGTAGTATAGTGACAGCTTTCCATGTTGAGATTCTCA 2880  
Db 2821 AGAAGCATGTTTGTACACTGCTTGTAGTATAGTGACAGCTTTCCATGTTGAGATTCTCA 2880  
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Db 2881 TATCATCTTGTATCTCTTAAAGTTTCATGTGAGTTTTTACCCTTAGGATGATTAAGATGTAT 2940  
QY 2941 ATAGGCAAAATCTTAAGTCTTCTCTACCTACATTTGTTTTCTTGGCTAGTAATAGTA 3000  
Db 2941 ATAGGCAAAATCTTAAGTCTTCTCTACCTACATTTGTTTTCTTGGCTAGTAATAGTA 3000  
QY 3001 GTAGTACTTCTGAAATAAATGTTCTCTCAAGATCTCTAAACCTCTGGAATAATATAA 3060  
Db 3001 GTAGTACTTCTGAAATAAATGTTCTCTCAAGATCTCTTAACCTCTTGGAAATATAA 3060  
QY 3061 AATATTGGCAAGAAAGAAAGTGTGTTTAAATATTTTTTAAATAATTTTTTAAATAAAG 3120  
Db 3061 AATATTGGCAAGAAAGAAAGTGTGTTTAAATATTTTTTAAATAATTTTTTAAATAAAG 3120  
QY 3121 AATCAGTAGGGTATAAATAGAAAGTTTAAATAATGCTCTCATAGAACGTCAGGGTTTACAT 3180  
Db 3121 AATCAGTAGGGTATAAATAGAAAGTTTAAATAATGCTCTCATAGAACGTCAGGGTTTACAT 3180  
QY 3181 TACAAGATTCTCACAAACCCCATTTGTAGAGTGAGTAAAGCATGTTACTACAGAGGAA 3240  
Db 3181 TACAAGATTCTCACAAACCCCATTTGTAGAGTGAGTAAAGCATGTTACTACAGAGGAA 3240  
QY 3241 AGTTTGAGAGTAAACCTGTAAAAATATATTTTTTGTGTACTTTCTTAAGAGAAAGAGTA 3300  
Db 3241 AGTTTGAGAGTAAACCTGTAAAAATATATTTTTTGTGTACTTTCTTAAGAGAAAGAGTA 3300  
QY 3301 TTGTTATGTTCTCCTTAACCTGTGTGATTAATGTTTAAAGTGATTTTCAATTTAAACATTT 3360  
Db 3301 TTGTTATGTTCTCCTTAACCTGTGTGATTAATGTTTAAAGTGATTTTCAATTTAAACATTT 3360  
QY 3361 GCAAAATTAATTTATTTTAAATTTTCTTTTGTAGATGAGTCTGCTTGTCTACCCAGG 3420  
Db 3361 GCAAAATTAATTTATTTTAAATTTTCTTTTGTAGATGAGTCTGCTTGTCTACCCAGG 3420  
QY 3421 CTGAGTGCAGTGGAGTATCTCTGCTACTGCAACCTCCGCCCTTCTGGGTTCAAGCAT 3480  
Db 3421 CTGAGTGCAGTGGAGTATCTCTGCTACTGCAACCTCCGCCCTTCTGGGTTCAAGCAT 3480  
QY 3481 TCTCTGCTCAGTCTCCTCAGTAGTGGAAATACAGGAGGTGCCACCATGCCCGACTA 3540  
Db 3481 TCTCTGCTCAGTCTCCTCAGTAGTGGAAATACAGGAGGTGCCACCATGCCCGACTA 3540  
QY 3541 ATTTTTTTTTTATTTTATAGAGACGGGTTTTCACCATGTTGGCCAGGCTGGTATCAAC 3600  
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QY 3601 TCCTGACCTCAAGAGATCCACTCGCCCTTGCCCTCCCAAGTGTCTGGATTACAGGCTTGA 3660  
Db 3601 TCCTGACCTCAAGAGATCCACTCGCCCTTGCCCTCCCAAGTGTCTGGATTACAGGCTTGA 3660  
QY 3661 GCCACACGCCCGGCTAAACATTTGCAAAATTTAAATGAGAGTTTTTAAATAATG 3720  
Db 3661 GCCACACGCCCGGCTAAACATTTGCAAAATTTAAATGAGAGTTTTTAAATAATG 3720  
QY 3721 ACTGCCCTGTTTCTGTTTTAGTATGTAATCTCAGTTCTTCCCTTGCACGTCTGCTGCC 3780  
Db 3721 ACTGCCCTGTTTCTGTTTTAGTATGTAATCTCAGTTCTTCCCTTGCACGTCTGCTGCC 3780  
QY 3781 ACTTAGTTTGGTTATATAGTCAATTAATGCTGCTGTCTGTAGTCTAGACTTTAAAT 3840  
Db 3781 ACTTAGTTTGGTTATATAGTCAATTAATGCTGCTGTGTAGTCTAGACTTTAAAT 3840  
QY 3841 TTAAGTTTCTTACAAGGGGAGAAAGTGTAAAAATTTTTTAAATAATGTTTTTCCAGGACA 3900  
Db 3841 TTAAGTTTCTTACAAGGGGAGAAAGTGTAAAAATTTTTTAAATAATGTTTTTCCAGGACA 3900

Qy 3901 CTTCACTTCCAAAGTCAGTAGAGTCTCAATCTAGTTGTTAGCCCAAGGACTCAAGACTG 3960  
Db 3901 CTTCACTTCCAAAGTCAGTAGAGTCTCAATCTAGTTGTTAGCCCAAGGACTCAAGACTG 3960  
Qy 3961 AATTGTTTAAACATAAGGCTTTCTGTTCTGGGAGCCGCACCTCAATTAATAATCTTCTA 4020  
Db 3961 AATTGTTTAAACATAAGGCTTTCTGTTCTGGGAGCCGCACCTCAATTAATAATCTTCTA 4020  
Qy 4021 AAACCTGTATGTTAGAGTTAAGCAAGACTTTTCTCTCTCTCCATCAGTGTGGAAT 4080  
Db 4021 AAACCTGTATGTTAGAGTTAAGCAAGACTTTTCTCTCTCTCCATCAGTGTGGAAT 4080  
Qy 4081 TTAATGCAACAAGCTGTAGTGGCTAACCAAGTTTATTTAAGAATTTGTTAGAAATGCTGT 4140  
Db 4081 TTAATGCAACAAGCTGTAGTGGCTAACCAAGTTTATTTAAGAATTTGTTAGAAATGCTGT 4140  
Qy 4141 TGCTTCAGGTTCTTAAATCACTCAGCACTCCAACCTTCTTAATCAAAATTTTGGAGACTTA 4200  
Db 4141 TGCTTCAGGTTCTTAAATCACTCAGCACTCCAACCTTCTTAATCAAAATTTTGGAGACTTA 4200  
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Db 4201 ACAGCATTTGCTGTGTTGAACATAAAGACACCGGATCTTTTCCATCTAATTCGCCA 4260  
Qy 4261 AAAATGATCATTTGCAAAAGTCAAACTATAGCCATATCCAAATCTTTCCCTCCCA 4320  
Db 4261 AAAATGATCATTTGCAAAAGTCAAACTATAGCCATATCCAAATCTTTCCCTCCCA 4320  
Qy 4321 GAGTCTCAGTGTCTACATGTAGACTATCTTCTCTGTATAAAGTTCACCTAGGATTT 4380  
Db 4321 GAGTCTCAGTGTCTACATGTAGACTATCTTCTCTGTATAAAGTTCACCTAGGATTT 4380  
Qy 4381 CAAGTCACCACTTATTTACATTTTAGTCATGCAAGATTCGAAGTGTTCGAATAAGT 4440  
Db 4381 CAAGTCACCACTTATTTACATTTTAGTCATGCAAGATTCGAAGTGTTCGAATAAGT 4440  
Qy 4441 ACTTATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCAATTTTAAATTTTGAG 4500  
Db 4441 ACTTATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCAATTTTAAATTTTGAG 4500  
Qy 4501 AACTGGTTTTAGCATTTACAACTAAATCCAGTTAATTAATATAGCTTATATTC 4560  
Db 4501 AACTGGTTTTAGCATTTACAACTAAATCCAGTTAATTAATATAGCTTATATTC 4560  
Qy 4561 TTTCTGCTACATTTGGTTTTTCCCTGTCCTTTGATTACGGGCTAAGGTAGGTAAG 4620  
Db 4561 TTTCTGCTACATTTGGTTTTTCCCTGTCCTTTGATTACGGGCTAAGGTAGGTAAG 4620  
Qy 4621 ANNGGCTAGTGTATATAATGATTTGGCCCTGTGTATATGATATTTTGTAT 4680  
Db 4621 ANNGGCTAGTGTATATAATGATTTGGCCCTGTGTATATGATATTTTGTAT 4680  
Qy 4681 TTTTGTCTTATATATTTACATTTTACATTTTGTGTTTCCATTTTAGGGAT 4740  
Db 4681 TTTTGTCTTATATATTTACATTTTACATTTTGTGTTTCCATTTTAGGGAT 4740  
Qy 4741 AAAATTTGATTTGAACATGATGAGACTACCGCCCAAGCACTTACATGATA 4800  
Db 4741 AAAATTTGATTTGAACATGATGAGACTACCGCCCAAGCACTTACATGATA 4800  
Qy 4801 TACCTTTAAACCCGAATCATTTGTTTATTTCCCTGATTACAGGTGTGAATGGGAAA 4860  
Db 4801 TACCTTTAAACCCGAATCATTTGTTTATTTCCCTGATTACAGGTGTGAATGGGAAA 4860  
Qy 4861 GGGGCTAGTATACAGTAGGATATACATGAGGATGATATATATCATTCGTTAGAGAA 4920  
Db 4861 GGGGCTAGTATACAGTAGGATATACATGAGGATGATATATATCATTCGTTAGAGAA 4920  
Qy 4921 ATGAATAAATGGGCTGGGCTCAGTGGCTCAGCGCTGTAATCCAGCACTTTGGGAGG 4980  
Db 4921 ATGAATAAATGGGCTGGGCTCAGTGGCTCAGCGCTGTAATCCAGCACTTTGGGAGG 4980

Qy 4981 CTGAGGCGAGTGGATCAGGAGTCTGAGAGATCGAGACCATCTGCTTAACACGGTGAAC 5040  
Db 4981 CTGAGGCGAGTGGATCAGGAGTCTGAGAGATCGAGACCATCTGCTTAACACGGTGAAC 5040  
Qy 5041 CCCGTCTCTACTAAAAACAGAAAATTAGCCGGCGTGGTGGCGGGCCCTGTAGTCCCA 5100  
Db 5041 CCCGTCTCTACTAAAAACAGAAAATTAGCCGGCGTGGTGGCGGGCCCTGTAGTCCCA 5100  
Qy 5101 GCTACTCCGGAGGCTGAGGAGGAGAAATGGTGTGAACCCGGGAGGACAGCTTGCAGTGA 5160  
Db 5101 GCTACTCCGGAGGCTGAGGAGGAGAAATGGTGTGAACCCGGGAGGACAGCTTGCAGTGA 5160  
Qy 5161 GCCGAGATCTCGCCACTGCACCTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAA 5220  
Db 5161 GCCGAGATCTCGCCACTGCACCTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAA 5220  
Qy 5221 AAAAAAAG 5232  
Db 5221 AAAAAAAG 5232

RESULT 2  
AAK89468  
ID AAK89468 standard; DNA; 8763 BP.  
XX AAK89468;  
XX AC  
XX XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3044.  
XX  
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;  
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;  
KW digestive system disorder; Meckel's diverticulum; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200155314-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01324.  
XX  
PR 31-JAN-2000; 2000US-0179055.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.



[illegible]

Qy 4744 ATTTGTTATTTTGAACATATGAATGAGACTACCGCCCGAGCAATTAGTTTCACATGATATAC 4803  
Db 2400 ATTTGTTATTTGAACATATGAATGAGACTACCGCCCGAGCAATTAGTTTCACATGATATAC 2459  
Qy 4804 CCTTTAAACCCGAATCATGTTGTTTATTTTCGATTTACACAGGTGTTGAATGGGAAAGG 4863  
Db 2460 CCTTTAAACCCGAATCATGTTGTTTATTTTCCTGATTACACAGGTGTTGAATGGGAAAGG 2519  
Qy 4864 GCTAGTATACAGTAGGATATACATGAGGATGGATGTATATATATATCATGCTGTTAGAGAAATG 4923  
Db 2520 GCTAGTATATCAGTAGGATATACATGAGGATGGATGTATATATATATCATGCTGTTAGAGAAATG 2579  
Qy 4924 AAATAAAATGGGCTGGGCTCAGTGGCTCAGCGCCTGTAATCCAGCACTTTGGGAGGCTG 4983  
Db 2580 AAATAAAATGGGCTGGGCTCAGTGGCTCAGCGCCTGTAATCCAGCACTTTGGGAGGCTG 2639  
Qy 4984 AGGAGGTGGATCAGAGGTGAGAGATCGAGACCATCTCGGTAAACACGGTGAACACCC 5043  
Db 2640 AGGAGGTGGATCAGAGGTGAGAGATCGAGACCATCTCGGTAAACACGGTGAACACCC 2699  
Qy 5044 GTCTCTACTAAACAAACAGAAATTAGCGGCGGTGGTGGCGGCGCCTGTAGTCCCGACT 5103  
Db 2700 GTCTCTACTAAACAAACAGAAATTAGCGGCGGTGGTGGCGGCGCCTGTAGTCCCGACT 2759  
Qy 5104 ACTCGGAGGCTGAGGAGGAGAAATGTTGTAACCCGGGAGGAGAGCTTGCAGTGAAGCC 5163  
Db 2760 ACTCGGAGGCTGAGGAGGAGAAATGTTGTAACCCGGGAGGAGAGCTTGCAGTGAAGCC 2819  
Qy 5164 GAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAAA 5223  
Db 2820 GAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAAA 2879  
Qy 5224 AAAAAA 5230  
Db 2880 AAAAAA 2886  
RESULT 3  
ID ABK93875 standard; cDNA; 3000 BP.  
XX  
AC ABK93875;  
XX  
DT 26-AUG-2002 (first entry)  
XX  
DE Human cDNA encoding inhibitor of apoptosis, XIAP #2.  
XX  
KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
KW pancreatic cancer; embryonic development; viral pathogenesis;  
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
KW lupus erythematosus; herpes virus infection; pox virus infection;  
KW adenovirus infection; proliferative disease.  
XX  
OS Homo sapiens.  
XX  
XX W0200226968-A2.  
XX  
XX 04-APR-2002.  
XX  
XX 27-SEP-2001; 2001WO-CA01379.  
XX  
XX 28-SEP-2000; 2000US-0672717.  
XX  
XX (UYOT-) UNIV OTTAWA.  
XX (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
XX  
XX WPI; 2002-479562/51.  
XX  
XX Novel antisense inhibitor of apoptosis nucleic acid useful for

enhancing apoptosis in a cell, for treating cancer and other  
proliferative diseases -  
Example 2; Fig 15; 135pp; English.  
XX  
The invention relates to an inhibitor of apoptosis (IAP) antisense  
nucleic acid (I) that inhibits IAP biological activity, regardless of  
length of the antisense nucleic acid, the IAP proteins may be mouse  
or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
composition comprising a mammalian IAP antisense molecule and a method of  
enhancing apoptosis in a cell, comprising administering a negative  
regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
antisense inhibitor is useful for enhancing apoptosis in a cell in a  
mammal diagnosed with a proliferative disease. The method is useful for  
treating a patient diagnosed with a proliferative disease like cancer.  
The IAP antisense molecule is useful to treat, ameliorate, improve,  
sustain or prevent proliferative diseases (e.g. ovarian cancer,  
adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
conditions where apoptosis is involved or implicated (e.g. embryonic  
development, viral pathogenesis, autoimmune disorders, neurodegenerative  
diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
virus, pox virus and adenovirus). The present sequence is a human IAP  
cDNA sequence.  
SQ Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;  
Query Match 43.5%; Score 2278; DB 24; Length 3000;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GAAAGGTGGCAAGTCCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Db 657 GAAAGGTGGCAAGTCCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT 716  
Qy 61 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAATTTGTAGAGAGTTTAATAGA 120  
Db 717 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAATTTGTAGAGAGTTTAATAGA 776  
Qy 121 TTAATAACTTTTGTCTAATTTTCCCAAGTGTAGTCTGTTTCCAGCATCAACACTGCACGA 180  
Db 777 TTAATAACTTTTGTCTAATTTTCCCAAGTGTAGTCTGTTTCCAGCATCAACACTGCACGA 836  
Qy 181 GCAGGGTTTCTTTTACTGGTGAAGGAGATACCGTGCGGTGTCTTTAGTTGTGCATGCAGCT 240  
Db 837 GCAGGGTTTCTTTTACTGGTGAAGGAGATACCGTGCGGTGTCTTTAGTTGTGCATGCAGCT 896  
Qy 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCAAAAT 300  
Db 897 GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCAAAAT 956  
Qy 301 TGCAGATTTATCAACGGCTTTTATCTTCAAAATAGTCCACGCGAGTCTACAAATTTCTGCT 360  
Db 957 TGCAGATTTATCAACGGCTTTTATCTTCAAAATAGTCCACGCGAGTCTACAAATTTCTGCT 1016  
Qy 361 ATCCAGATGTCTCAGTACAAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGCCTTA 420  
Db 1017 ATCCAGATGTCTCAGTACAAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGCCTTA 1076  
Qy 421 GACAGGCCATCTGACACACATGCAGACTATCTTTTGAAGACTGGGCAGGTTGTAGATATA 480  
Db 1077 GACAGGCCATCTGACACACATGCAGACTATCTTTTGAAGACTGGGCAGGTTGTAGATATA 1136  
Qy 481 TCAGACACCATATACCCGAGGAACCCCTCCATGTATCTAGAGAGCTAGATTAAGTCC 540  
Db 1137 TCAGACACCATATACCCGAGGAACCCCTCCATGTATCTAGAGAGCTAGATTAAGTCC 1196  
Qy 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Db 1197 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 1256  
Qy 601 TACTACACAGGTATGGTGACCAAGTGCAGTCTTTTCTGTGGTGGAAAACTGAAAAAT 660  
Db 1257 TACTACACAGGTATGGTGACCAAGTGCAGTCTTTTCTGTGGTGGAAAACTGAAAAAT 1316



QY 661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTTCCTAAATTGCTTCTTT 720  
DB 1317 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTTCCTAAATTGCTTCTTT 1376  
QY 721 GTTTTGGCGGGAATCTTAATATTCGAAGTGAATCGATGCTGAGTTCGTATAGGAAT 780  
DB 1377 GTTTTGGCGGGAATCTTAATATTCGAAGTGAATCGATGCTGAGTTCGTATAGGAAT 1436  
QY 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTAATCAAGCACGGATC 840  
DB 1437 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTAATCAAGCACGGATC 1496  
QY 841 TTTTACTTTTGGGACATGGATATACCTTAACCAAGGAGCAGCTTGCAGAGCTGGATTT 900  
DB 1497 TTTTACTTTTGGGACATGGATATACCTTAACCAAGGAGCAGCTTGCAGAGCTGGATTT 1556  
QY 901 TATGCTTTAGGTGAAGTGATATAAGTAAAGTGTCTTCTACTGTGGAGGAGGCTAACTGAT 960  
DB 1557 TATGCTTTAGGTGAAGTGATATAAGTAAAGTGTCTTCTACTGTGGAGGAGGCTAACTGAT 1616  
QY 961 TGGAGCCCGACGTAAGACCTTGGCAACAACATGCTAAATGGTATCCAGGGTGCAAAATAT 1020  
DB 1617 TGGAGCCCGACGTAAGACCTTGGCAACAACATGCTAAATGGTATCCAGGGTGCAAAATAT 1676  
QY 1021 CTGTTTAGAACAGAGGACAAAGATATATAACAATATTTCAATTTAACTCACTTTCAG 1080  
DB 1677 CTGTTTAGAACAGAGGACAAAGATATATAACAATATTTCAATTTAACTCACTTTCAG 1736  
QY 1081 GAGTGTCTGGTAAAGTACTGAGAAAAACACCATCACTAACTAGAGAAATATGATGATACC 1140  
DB 1737 GAGTGTCTGGTAAAGTACTGAGAAAAACACCATCACTAACTAGAGAAATATGATGATACC 1796  
QY 1141 ATCTTTCCAAATCCATGCTGTAACAAGCTATACCAATGGGGTTCAGTTTCAAGGACATTT 1200  
DB 1797 ATCTTTCCAAATCCATGCTGTAACAAGCTATACCAATGGGGTTCAGTTTCAAGGACATTT 1856  
QY 1201 AAGAAATAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTCAGGTT 1260  
DB 1857 AAGAAATAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTCAGGTT 1916  
QY 1261 CTGGTTGCAGATCTAGTGAAGTCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320  
DB 1917 CTGGTTGCAGATCTAGTGAAGTCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1976  
QY 1321 TCATTTACAGAAAGATAGTACTCAAGAGCAGCTAAGCGCCTCAAGAGGAGAGCTT 1380  
DB 1977 TCATTTACAGAAAGATAGTACTCAAGAGCAGCTAAGCGCCTCAAGAGGAGAGCTT 2036  
QY 1381 TGCAAAATCTGATGATAGAAATATGCTATCGTTTTTGTCTTGTGGACATCTAGTC 1440  
DB 2037 TGCAAAATCTGATGATAGAAATATGCTATCGTTTTTGTCTTGTGGACATCTAGTC 2096  
QY 1441 ACTTTGAACAAATGCTGAGGACGTTGACAAAGTGTCCCATGTGTCACAGTCAATACT 1500  
DB 2097 ACTTTGAACAAATGCTGAGGACGTTGACAAAGTGTCCCATGTGTCACAGTCAATACT 2156  
QY 1501 TTTCAGCAAAAATTTTATGCTTTAAATCTACTCTATAGTGGCATGTTATGTTGTTCT 1560  
DB 2157 TTTCAGCAAAAATTTTATGCTTTAAATCTACTCTATAGTGGCATGTTATGTTGTTCT 2216  
QY 1561 TATTACCCTGATTTGATGTGATGTGAACGACTGACTTTAAGTAATCAGGATTTGAATTCCTAT 1620  
DB 2217 TATTACCCTGATTTGATGTGATGTGAACGACTGACTTTAAGTAATCAGGATTTGAATTCCTAT 2276  
QY 1621 TAGCATTTGCTACCAAGTAGGAAAAAAATGTACATGCGAGTGTGTTTATGTTGGCAATATA 1680  
DB 2277 TAGCATTTGCTACCAAGTAGGAAAAAAATGTACATGCGAGTGTGTTTATGTTGGCAATATA 2336  
QY 1681 ATCTTTGAAATTTCTGATTTTTCAGGCTATAGCTGCTATATCCATTTTCTTACTGTATA 1740  
DB 2337 ATCTTTGAAATTTCTGATTTTTCAGGCTATAGCTGCTATATATCCATTTTCTTACTGTATA 2396

QY 1741 TTTAATTTGAAACCATAGACTAAGAATAAAGACATCATACTATACTGAACAAATGTGT 1800  
DB 2397 TTTAATTTGAAACCATAGACTAAGAATAAAGACATCATACTATACTGAACAAATGTGT 2456  
QY 1801 ATTCATAGTATACTGATTTAATTTCTAAGTGTAAAGTAATTAATCATCTGGATTTTAT 1860  
DB 2457 ATTCATAGTATACTGATTTAATTTCTAAGTGTAAAGTAATTAATCATCTGGATTTTAT 2516  
QY 1861 TCTTTTTCAGATPAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTTAGAGTTA 1920  
DB 2517 TCTTTTTCAGATPAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTTAGAGTTA 2576  
QY 1921 ATCTCCCAATCACATAATTTGTTTGTGAAAAAGGAATAAATTTGTTCCATGCTGGTG 1980  
DB 2577 ATCTCCCAATCACATAATTTGTTTGTGAAAAAGGAATAAATTTGTTCCATGCTGGTG 2636  
QY 1981 GAAAGATAGAGATTTGTTTGTAGAGTTGGTTGTTGTTTGTGTTTGTGTTTGTGTTTGT 2040  
DB 2637 GAAAGATAGAGATTTGTTTGTAGAGTTGGTTGTTGTTTGTGTTTGTGTTTGTGTTTGT 2696  
QY 2041 TTTAAAGTTATAAACACAGTACTTGTGCGAATTTATTTTAAAGTGATTTGCCATTTTGT 2100  
DB 2697 TTTAAAGTTATAAACACAGTACTTGTGCGAATTTATTTTAAAGTGATTTGCCATTTTGT 2756  
QY 2101 AAAGCTATTTAATGATAGATATCTGAGCCAACTGACTGACATGGAAGATGTCA 2160  
DB 2757 AAAGCTATTTAATGATAGATATCTGAGCCAACTGACTGACATGGAAGATGTCA 2816  
QY 2161 AGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA 2220  
DB 2817 AGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA 2876  
QY 2221 AAGTATGATGTTTAAATATCATAGAACAAAGATTTGGAAGATATACACCAAACTG 2280  
DB 2877 AAGTATGATGTTTAAATATCATAGAACAAAGATTTGGAAGATATACACCAAACTG 2936  
QY 2281 TTAATGTGGTTTCTCTTCGGGGAGGGGGGATTTGGGGAGGGGGCCCCA 2329  
DB 2937 TTAATGTGGTTTCTCTTCGGGGAGGGGGGATTTGGGGAGGGGGCCCCA 2985  
RESULT 4  
AAK99405 ID AAK99405 standard; DNA; 2404 BP.  
XX AC AAK99405;  
XX DT 27-JUN-2002 (first entry)  
XX DE DNA of APP related human homologue hCP35211.  
XX KW Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;  
KW amyloid precursor protein; tissue-specific expression control; human APP;  
KW APP pathway modulator; gene therapy; gene; ds.  
XX OS Homo sapiens.  
XX FH Key  
XX FT CDS 692..1528  
XX FT /\*tag= a  
XX FT /product= "protein of human homologue hCP35211"  
XX FT /note= "No start codon"  
PN WO200226820-A2.  
PD 04-APR-2002.  
XX 01-OCT-2001; 2001WO-EP11345.  
XX 29-SEP-2000; 2000US-236893P.  
XX 14-JUN-2001; 2001US-298309P.  
XX (NOVS ) NOVARTIS AG.





QY	1680	AAATCTTTTGAATTCCTTGATTTTTTTCAGGGTATTAGCTGPAATATCCATTTTTTTTTTACTGGTT	1739
Db	1681	AAATCTTTTGAATTCCTTGATTTTTTTCAGGGTATTAGCTGPAATATCCATTTTTTTTTTACTGGT	1740
QY	1740	ATTAAATCTGAACCATAGACTAGAAATAGAAGCATCATATAACTGAACACAATGTG	1799
Db	1741	ATTAAATCTGAACCATAGACTAAGAATAGAAGCATCATATAACTGAACACAATGTG	1800
QY	1800	TATTCATAGTACTAGATTAAATTTCTAAGTGAAGTGAATTAATCATCTGGGATTTTTTAA	1859
Db	1801	TATTCATAGTACTAGATTAAATTTCTAAGTGAAGTGAATTAATCATCTGGGATTTTTTAA	1860
QY	1860	TTCTTTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATAAATATGGAGATTAGAGTT	1919
Db	1861	TTCTTTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATAAATATGGAGATTAGAGTT	1920
QY	1920	AATCTCCCCAATCACATAATTTGTTGTGTGAAAGGAATAAATTTGTTCCATGCTGGT	1979
Db	1921	AATCTCCCCAATCACATAATTTGTTGTGTG - AAAAGGAATAAATTTGTTCCATGCTGGT	1979
QY	1980	GGAAGCATAGAGATTGTTTTTAGAGGTGGTTGTTGCTTTTAGGATTCTGTCTCCATTTTC	2039
Db	1980	GGAAGCATAGAGATTGTTTTTAGAGGTGGTTGTTGCTTTTAGGATTCTGTCTCCATTTTC	2039
QY	2040	TTTTAAAGTTATAAACACGCTACTTCTGCGAATTAATTTTTTAAAGTGATTTGCCATTTTT	2099
Db	2040	TTTTAAAGTTATAAACACGCTACTTCTGCGAATTAATTTTTTAAAGTGATTTGCCATTTTT	2099
QY	2100	GAAAGCGTATTAAATGATAGATACTATCTGAGCCACACATGACTGACATGGAAGATGTC	2159
Db	2100	GAAAGCGTATTAAATGATAGATACTATCTGAGCCACACATGACTGACATGGAAGATGTC	2159
QY	2160	AAAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATGCTGAGCCAGATC	2219
Db	2160	AAAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATGCTGAGCCAGATC	2219
QY	2220	AAAGTATGATGTTTTTAATATGCATAGAACAAAAGATTTTGGAAAGATATACACCAAAC	2279
Db	2220	AAAGTATGATGTTTTTAATATGCATAGAACAAAAGATTTTGGAAAGATATACACCAAAC	2279
QY	2280	GTTAAATGCGTTTCTCTCGGGGAGGGGGGATTGGGGG	2319
Db	2280	GTTAAATGCGTTTCTCTCTCGGGGAGGGGGGATTGGGGG	2319
RESULT 5			
AAAT70836			
ID	AAAT70836 standard; cDNA; 2540 BP.		
XX	XX		
AC	AAAT70836;		
XX	XX		
DT	02-SEP-1997 (first entry)		
XX	XX		
DE	Human apoptosis inhibitor xiap cDNA.		
XX	XX		
KW	Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;		
KW	XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;		
KW	ischaemia; myocardial infarction; stroke;		
KW	reperfusion injury; toxin-induced liver disease; gene therapy;		
KW	diagnosis; ds.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
FH	Key		
CD	Location/Qualifiers		
FT	34..1527		
FT	/*tag= a		
XX	XX		
XX	XX		
PN	W09706255-A2.		
XX	XX		
PD	20-FEB-1997.		
XX	XX		
PF	05-AUG-1996; 96WO-IB01022.		

[illegible]

||||| 541 TTTTCAAACTGGCCAGACTATGCTCACTAACCCCAAGAGAGTTAGCAAGTGTGACTC 600  
||||| 601 TACTACACAGGTATGGTGACCAAGTGCAGTGTCTTTGTTGGTGSTGGAAACATGAAAAAT 660  
||||| 601 TACTACACAGGTATGGTGACCAAGTGCAGTGTCTTTGTTGGTGSTGGAAACATGAAAAAT 660  
||||| 661 TGGGAACCTTGTGATCGTGGCTGGTCAGAACACAGCGCACACTTCCCTAATTCCTCTTTT 720  
||||| 661 TGGGAACCTTGTGATCGTGGCTGGTCAGAACACAGCGCACACTTCCCTAATTCCTCTTTT 720  
||||| 721 GTTTTGGCGGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTTGATAGAAT 780  
||||| 721 GTTTTGGCGGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTTGATAGAAT 780  
||||| 781 TTCCCAAAATTCACAAATCTTCCAAGAAATCCATCCATGSCAGATTATGAAGCACGGATC 840  
||||| 781 TTCCCAAAATTCACAAATCTTCCAAGAAATCCATCCATGSCAGATTATGAAGCACGGATC 840  
||||| 841 TTTTACTTTTGGGACATGGATATACTCAGTTTAAACAAGGAGCAGCTTGCAGAGCTGGATTT 900  
||||| 841 TTTTACTTTTGGGACATGGATATACTCAGTTTAAACAAGGAGCAGCTTGCAGAGCTGGATTT 900  
||||| 901 TATGCTTTTAGTGAAGTGATAAAGTAAAGTGCTTTTCACTGTGGAGGAGGCTTAACGTGAT 960  
||||| 901 TATGCTTTTAGTGAAGTGATAAAGTAAAGTGCTTTTCACTGTGGAGGAGGCTTAACGTGAT 960  
||||| 961 TGGAAAGCCAGTGAAGACCTTGGGACACACATGCTAAATGGTATCCAGGGTGCAAAATAT 1020  
||||| 961 TGGAAAGCCAGTGAAGACCTTGGGACACACATGCTAAATGGTATCCAGGGTGCAAAATAT 1020  
||||| 1021 CTGTTAGAACAAGGAGCAGAAATATATAACAATATTCATTAACTCACTTCACTTGAG 1080  
||||| 1021 CTGTTAGAACAAGGAGCAGAAATATATAACAATATTCATTAACTCACTTCACTTGAG 1080  
||||| 1081 GAGTGTCTGTGAAGAACTACTGAGAAACACCACATCACTAACTAGAAATTTGATGATACC 1140  
||||| 1081 GAGTGTCTGTGAAGAACTACTGAGAAACACCACATCACTAACTAGAAATTTGATGATACC 1140  
||||| 1141 ATCTTCCAAATCCTATGGTACAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATT 1200  
||||| 1141 ATCTTCCAAATCCTATGGTACAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATT 1200  
||||| 1201 AAGAAATAATGGAGGAAAAATTCAGATATCTGGGAGCACTATAAATCACTTGAGGTT 1260  
||||| 1201 AAGAAATAATGGAGGAAAAATTCAGATATCTGGGAGCACTATAAATCACTTGAGGTT 1260  
||||| 1261 CTGTTGTCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT 1320  
||||| 1261 CTGTTGTCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT 1320  
||||| 1321 TCATTACAGAAAGAGATTACTAGAGACAGCTAAGGCGCCTGCAAGAGGAGAAGCTT 1380  
||||| 1321 TCATTACAGAAAGAGATTACTAGAGACAGCTAAGGCGCCTGCAAGAGGAGAAGCTT 1380  
||||| 1381 TGCAAAATCTGTATGGATAGAAATATTCGTATCGTTTTTGTCTTGTGACATCTAGTC 1440  
||||| 1381 TGCAAAATCTGTATGGATAGAAATATTCGTATCGTTTTTGTCTTGTGACATCTAGTC 1440  
||||| 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT 1500  
||||| 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT 1500  
||||| 1501 TTCAAGCAAAAAATTTTATGCTCTTAATCTAACTCTATAGTAGGCATGTTATGTTCT 1560  
||||| 1501 TTCAAGCAAAAAATTTTATGCTCTTAATCTAACTCTATAGTAGGCATGTTATGTTCT 1560  
||||| 1561 TATTACCTGATTGAATGTGTGATGCAACTGACTTTTAAGTAAATCAGAGATTGAATCCAT 1620  
||||| 1561 TATTACCTGATTGAATGTGTGATGCAACTGACTTTTAAGTAAATCAGAGATTGAATCCAT 1620  
||||| 1621 TAGCATTTGCTACCAAGTAGGAAAAAAATGTATCATGGCAGTGTGTTAGTTGGCAATATA 1680  
|||||

Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAAATGTATCATGGCAGTGTGTTAGTTGGCAATATA 1680  
QY 1681 ATCTTTGAAATTTCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTCTTACTGTTA 1740  
Db 1681 ATCTTTGAAATTTCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTCTTACTGTTA 1740  
QY 1741 TTTAATTTGAAACCATAGACTAAGAATAAAGAGCATCATATAAATCTGAACACAATGCT 1800  
Db 1741 TTTAATTTGAAACCATAGACTAAGAATAAAGAGCATCATATAAATCTGAACACAATGCT 1800  
QY 1801 ATTCATAGTATAGTAAATTTCTAAGTGTAAAGTGAATTAATCATCTGGATTTTAT 1860  
Db 1801 ATTCATAGTATAGTAAATTTCTAAGTGTAAAGTGAATTAATCATCTGGATTTTAT 1860  
QY 1861 TCTTTTCAGATAGCTTAAACAAATGGAGCTTCTGTATATAAAATGTGGAGATTAGAGTTA 1920  
Db 1861 TCTTTTCAGATAGCTTAAACAAATGGAGCTTCTGTATATAAAATGTGGAGATTAGAGTTA 1920  
QY 1921 ATCTCCCAATACATAAATTTGTTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCAATACATAAATTTGTTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980  
QY 1981 GAAAGATAGAGATTGTTTTAGAGGTTGGTGTGTTGTTTTAGGATTCGTGCCATTTTCT 2040  
Db 1981 GAAAGATAGAGATTGTTTTAGAGGTTGGTGTGTTGTTTTAGGATTCGTGCCATTTTCT 2040  
QY 2041 T 2041  
Db 2041 T 2041  
  
RESULT 6  
AAA64901  
ID AAA64901 standard; DNA; 2540 BP.  
XX  
AC AAA64901;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE Human X-linked inhibitor of apoptosis DNA.  
XX  
KW X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880;  
KW antisense; antiinflammatory; cytostatic; tumour; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 34..1527  
FT /\*tag= a  
FT /product= "X-linked inhibitor of apoptosis"  
XX  
PN US6087173-A.  
XX  
PD 11-JUL-2000.  
XX  
PF 09-SEP-1999; 99US-0392580.  
XX  
PR 09-SEP-1999; 99US-0392580.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Bennett CF, Cowser LM, Ackermann EJ;  
DR WPI; 2000-498201/44.  
DR P-PSDB; AAY99985.  
XX  
PT Antisense compound useful for research reagents, diagnostics,  
PT prophylaxis and for treating disorders associated with X-linked  
PT inhibitor of apoptosis, modulates expression of X-linked inhibitor of  
PT apoptosis -  
XX  
PS Example 13; Column 43-48; 33pp; English.  
XX

CC The present invention relates to antisense oligonucleotides designed to  
CC inhibit expression of the human x-linked inhibitor of apoptosis. The  
CC present sequence is the x-linked inhibitor of apoptosis DNA.  
CC Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are  
CC more effective inhibitors than unmodified oligonucleotides. The  
CC oligonucleotides may be used to inhibit x-linked inhibitor of apoptosis  
CC expression in cells and tissues in vitro. The oligonucleotides are also  
CC useful for treating animals or humans, prone to a disease associated  
CC with x-linked inhibitor of apoptosis. The oligonucleotides may also be  
CC used prophylactically to prevent infection, inflammation or tumour  
CC formation.  
XX

SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;

Query Match 38.0%; Score 1990; DB 21; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GAAGAAGGTGGACAGTCTCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT	60
Db	1	GAAGAAGGTGGACAGTCTCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT	60
Qy	61	AAACCTTCTGTACCTGCAGACATCAATTAAGGAAGAAGATTTGTAGAGAGCTTTAATAGA	120
Db	61	AAACCTTCTGTACCTGCAGACATCAATTAAGGAAGAAGATTTGTAGAGAGCTTTAATAGA	120
Qy	121	TAAAACTTTTGGCTAATTTTCCAAAGTGGTAGTCTCTTTCCAGCATCAACACTGCGACGA	180
Db	121	TAAAACTTTTGGCTAATTTTCCAAAGTGGTAGTCTCTTTCCAGCATCAACACTGCGACGA	180
Qy	181	CGAGGGTTCTTTATCTAGTGGTGAAGGAGATACCGTGCAGTCTTTAGTGTCTAGTGCAGCT	240
Db	181	CGAGGGTTCTTTATCTAGTGGTGAAGGAGATACCGTGCAGTCTTTAGTGTCTAGTGCAGCT	240
Qy	241	GTAGATAGTGCATATGGAGATCGACAGTTCGAAAGTGGAGACAGAGATATCCCAAT	300
Db	241	GTAGATAGTGCATATGGAGATCGACAGTTCGAAAGTGGAGACAGAGATATCCCAAT	300
Qy	301	TGCAGATTTATCAAGGGCTTTTATCTTGAATAATAGTGCAGCGAGTCTACAAATCTCGT	360
Db	301	TGCAGATTTATCAAGGGCTTTTATCTTGAATAATAGTGCAGCGAGTCTACAAATCTCGT	360
Qy	361	ATCCAGAATGGTCAAGATGACAAAGTTGAAACATATCTGGGAAGCAGAGATCATTTGGCCCTTA	420
Db	361	ATCCAGAATGGTCAAGATGACAAAGTTGAAACATATCTGGGAAGCAGAGATCATTTGGCCCTTA	420
Qy	421	GACAGGCCATCTGACACACATGCACTATCTTTTGAAACTGGGCGAGTTGTAGATATA	480
Db	421	GACAGGCCATCTGACACACATGCACTATCTTTTGAAACTGGGCGAGTTGTAGATATA	480
Qy	481	TCAGACACATATACCCGAGGAACCTGCCATGTATAGTGAAGAAGCTAGATTAAGTCC	540
Db	481	TCAGACACATATACCCGAGGAACCTGCCATGTATAGTGAAGAAGCTAGATTAAGTCC	540
Qy	541	TTTCAGAACTGGCCAGACTATGCTCACTCAACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC	600
Db	541	TTTCAGAACTGGCCAGACTATGCTCACTCAACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC	600
Qy	601	TACTACACAGTATTTGGTACCAAGTGCAGTCTTTTGTGGTGGGAACTGAAAT	660
Db	601	TACTACACAGTATTTGGTACCAAGTGCAGTCTTTTGTGGTGGGAACTGAAAT	660
Qy	661	TGGGAACCTTGTGATCGTCTGGTGCAGACACAGGCGACACTTTCCCTAAATGCTTCTTT	720
Db	661	TGGGAACCTTGTGATCGTCTGGTGCAGACACAGGCGACACTTTCCCTAAATGCTTCTTT	720
Qy	721	GTCTTGGCCCGGAATCTTAAATATTCGAAGTGAATCTGATGCTGTGAGTCTCTAGGAAAT	780
Db	721	GTCTTGGCCCGGAATCTTAAATATTCGAAGTGAATCTGATGCTGTGAGTCTCTAGGAAAT	780
Qy	781	TTCCCAATTTCAACAAATCTTCCAGAAATCCATCCATGGCAGATTAAGACAGCGATC	840
Dh	781	TTCCCAATTTCAACAAATCTTCCAGAAATCCATCCATGGCAGATTAAGACAGCGATC	840

Qy	841	TTTACTTTTGGACATGGATATACTCAGTTAACAGGAGCAGCTTGCAGAGCTGGATT	900
Db	841	TTTACTTTTGGACATGGATATACTCAGTTAACAGGAGCAGCTTGCAGAGCTGGATT	900
Qy	901	TATGCTTTAGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGAGGAGGCTAACTGAT	960
Db	901	TATGCTTTAGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGAGGAGGCTAACTGAT	960
Qy	961	TGGAGCCCTGAGACCTTTGGGACCAACATGCTAAATGATGATCCAGGCTGCAAAAT	1020
Db	961	TGGAGCCCTGAGACCTTTGGGACCAACATGCTAAATGATGATCCAGGCTGCAAAAT	1020
Qy	1021	CTGTTAGAACAGAGGAGCAAGATATATAAACAATATTTTAACTCACTTCACTTGG	1080
Db	1021	CTGTTAGAACAGAGGAGCAAGATATATAAACAATATTTTAACTCACTTCACTTGG	1080
Qy	1081	GAGTGTCTGTTGTAAGACTTACTGAGAAAACACCATCACTAAGAAATTTGATGATACC	1140
Db	1081	GAGTGTCTGTTGTAAGACTTACTGAGAAAACACCATCACTAAGAAATTTGATGATACC	1140
Qy	1141	ATCTTCCAAATCCTATGTTACAAAGACTATACGAATGGGTTTCAGTTTCAAGGACAT	1200
Db	1141	ATCTTCCAAATCCTATGTTACAAAGACTATACGAATGGGTTTCAGTTTCAAGGACAT	1200
Qy	1201	AAGAAATTAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT	1260
Db	1201	AAGAAATTAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT	1260
Qy	1261	CTGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT	1320
Db	1261	CTGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT	1320
Qy	1321	TCATTACAGAAAGAGATTAGTACTGAAGCAGCTTAAGCGCCTGCAAGAGAGAGGCTT	1380
Db	1321	TCATTACAGAAAGAGATTAGTACTGAAGCAGCTTAAGCGCCTGCAAGAGAGAGGCTT	1380
Qy	1381	TGCAAAATCTGTATGGATAGAAATATTCCTATCGTTTTTGTTCCTTTGGACATCTAGTC	1440
Db	1381	TGCAAAATCTGTATGGATAGAAATATTCCTATCGTTTTTGTTCCTTTGGACATCTAGTC	1440
Qy	1441	ACTTGTAAACAAATGTGCTGAAGCAGTTCACAAGTGTCCCATGTGCTACACAGTCAAT	1500
Db	1441	ACTTGTAAACAAATGTGCTGAAGCAGTTCACAAGTGTCCCATGTGCTACACAGTCAAT	1500
Qy	1501	TTCAAGCAAAAATTTTATCTTAATCTAATCTAGTAGGCACTTATGTTGTTCT	1560
Db	1501	TTCAAGCAAAAATTTTATCTTAATCTAATCTAGTAGGCACTTATGTTGTTCT	1560
Qy	1561	TATTACCTGATTTGAATGTGATGTGAACCTGAACTTTAAGTAATCAGGATTTGAATTCAT	1620
Db	1561	TATTACCTGATTTGAATGTGATGTGAACCTGAACTTTAAGTAATCAGGATTTGAATTCAT	1620
Qy	1621	TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTAGTTGGCAATATA	1680
Db	1621	TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTAGTTGGCAATATA	1680
Qy	1681	ATCTTTGAATTTCTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTCTTACTGTTA	1740
Db	1681	ATCTTTGAATTTCTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTCTTACTGTTA	1740
Qy	1741	TTTAATTTGAAACCATAGACTAAGAAATAAGAGCATCATACTATAACTGAACACAAATGCT	1800
Db	1741	TTTAATTTGAAACCATAGACTAAGAAATAAGAGCATCATACTATAACTGAACACAAATGCT	1800
Qy	1801	ATTCATAGTATACGATTTAATTTCTAAGTGAAGTGAATTAATCACTCGGATTTTTTAT	1860
Db	1801	ATTCATAGTATACGATTTAATTTCTAAGTGAAGTGAATTAATCACTCGGATTTTTTAT	1860
Qy	1861	TCCTTTTCAGATAGCTTTAACAATGGAGCTTCTGTTATATAAATCTGGAGATTAGAGTTA	1920
Db	1861	TCCTTTTCAGATAGCTTTAACAATGGAGCTTCTGTTATATAAATCTGGAGATTAGAGTTA	1920

QY 1921 ATCTCCCAATCACATAATTTGTTTGTGTAAGAAAGAAATAATTTGCCATGCTGGTG 1980  
Db 1921 ATCTCCCAATCACATAATTTGTTTGTGTAAGAAAGAAATAATTTGCCATGCTGGTG 1980  
QY 1981 GAAAGATAGAGATGTTTTAGAGGTTGGTTGTTGTTTAGATTTCTGTCATTTTCT 2040  
Db 1981 GAAAGATAGAGATGTTTTAGAGGTTGGTTGTTGTTTAGATTTCTGTCATTTTCT 2040  
QY 2041 T 2041  
Db 2041 T 2041

RESULT 7  
ABK93869  
ID ABK93869 standard; cDNA; 2540 BP.  
XX  
AC ABK93869;  
XX  
DT 26-AUG-2002 (first entry)  
XX  
DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.  
XX  
KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
KW pancreatic cancer; embryonic development; viral pathogenesis;  
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
KW lupus erythematosus; herpes virus infection; pox virus infection;  
KW adenovirus infection; proliferative disease.  
XX  
OS Homo sapiens.  
XX  
XX WC200226968-A2.  
XX  
XX PD 04-APR-2002.  
XX  
XX PF 27-SEP-2001; 2001WO-CA01379.  
XX  
XX PR 28-SEP-2000; 2000US-067217.  
XX  
XX PA (UYOR-) UNIV OTTAWA.  
XX (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
XX PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
XX  
XX WPI; 2002-479562/51.  
DR P-PSDB; ABG65663.  
XX  
XX Novel antisense inhibitor of apoptosis nucleic acid useful for  
PT enhancing apoptosis in a cell, for treating cancer and other  
PT proliferative diseases -  
XX  
XX PS Disclosure; Fig 1; 135pp; English.  
XX  
XX The invention relates to an inhibitor of apoptosis (IAP) antisense  
CC nucleic acid (I) that inhibits IAP biological activity, regardless of  
CC length of the antisense nucleic acid, the IAP proteins may be mouse  
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
CC composition comprising a mammalian IAP antisense molecule and a method of  
CC enhancing apoptosis in a cell, comprising administering a negative  
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
CC mammal diagnosed with a proliferative disease. The method is useful for  
CC treating a patient diagnosed with a proliferative disease like cancer.  
CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
CC conditions where apoptosis is involved or implicated (e.g. embryonic  
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
CC virus, pox virus and adenovirus). The present sequence is a human IAP  
CC cDNA sequence.  
XX

SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;  
Query Match 37.6%; Score 1969; DB 24; Length 2540;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 2019; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 22 TTTCAGAGAGAGATGACCTTTTACAGCTTTTGAAGGATCTAAACTCTGTGTACCTGCAGAC 81  
Db 22 TTTCAGAGAGAGATGACCTTTTACAGCTTTTGAAGGATCTAAACTCTGTGTACCTGCAGAC 81  
QY 82 ATCAATAAGGAAGAATAATTTGTAGAAGAGTTTAAATAGATTAATAAATCTTTTGCTAAATTT 141  
Db 82 ATCAATAAGGAAGAATAATTTGTAGAAGAGTTTAAATAGATTAATAAATCTTTTGCTAAATTT 141  
QY 142 CCAAGTGGTAGTCCTGTTTCCAGCATCAACACTGCGCAGCAGGAGGTTTCTTTATACGGT 201  
Db 142 CCAAGTGGTAGTCCTGTTTCCAGCATCAACACTGCGCAGCAGGAGGTTTCTTTATACGGT 201  
QY 202 GAAGGAGATACCGTGGTGGTCTTTAGTTGTATGTCATGACCTGTAGATAGATGGCAATATGGA 261  
Db 202 GAAGGAGATACCGTGGTGGTCTTTAGTTGTATGTCATGACCTGTAGATAGATGGCAATATGGA 261  
QY 262 GACTCAGCAGTTGGAAGACACAGAGAAAGTATPCCCAATTTGCAGATTTATCAACGGCTTT 321  
Db 262 GACTCAGCAGTTGGAAGACACAGAGAAAGTATPCCCAATTTGCAGATTTATCAACGGCTTT 321  
QY 322 TATCTTGAATAATAGTCCAGCAGCTCTACAAATTTCTGGTATCCAGAAATGGTCAGTACAAA 381  
Db 322 TATCTTGAATAATAGTCCAGCAGCTCTACAAATTTCTGGTATCCAGAAATGGTCAGTACAAA 381  
QY 382 GTTGAAATATCTCTGGGAAGCAGAGATCATTTTGCCTTTAGACAGCCATCTGAGACACAT 441  
Db 382 GTTGAAATATCTCTGGGAAGCAGAGATCATTTTGCCTTTAGACAGCCATCTGAGACACAT 441  
QY 442 GCAGACTATCTTTTGAGAACTGGGCGAGGTTGTAGATATATCAGACACATATACCCGAGG 501  
Db 442 GCAGACTATCTTTTGAGAACTGGGCGAGGTTGTAGATATATCAGACACATATACCCGAGG 501  
QY 502 AACCTGCCATGTATAGTGAAGAGCTAGATTAAGTCTTTCAGAACTGGCCAGACTAT 561  
Db 502 AACCTGCCATGTATGTGAAGAGCTAGATTAAGTCTTTCAGAACTGGCCAGACTAT 561  
QY 562 GCTCACCTAACCCCAAGAGAGTTAGCAAGTGTCTGACTCTACTACAGAGTATTTGGTGAC 621  
Db 562 GCTCACCTAACCCCAAGAGAGTTAGCAAGTGTCTGACTCTACTACAGAGTATTTGGTGAC 621  
QY 622 CAAGTCAGTGTCTTTGTTGGTGGAAACTGAAAAATTTGGGAACCTTTGTGATCGTGCC 681  
Db 622 CAAGTCAGTGTCTTTGTTGGTGGAAACTGAAAAATTTGGGAACCTTTGTGATCGTGCC 681  
QY 682 TGGTCAACACACAGGCGACACTTTCCCTAATTTGCTTCTTTGTTGGGCGGGAATCTTAAT 741  
Db 682 TGGTCAACACACAGGCGACACTTTCCCTAATTTGCTTCTTTGTTGGGCGGGAATCTTAAT 741  
QY 742 ATTCGAAGTGAATCTGATGCTGTGAGTTCGTATAGGAATTTCCCAATTTCAACAAATCTT 801  
Db 742 ATTCGAAGTGAATCTGATGCTGTGAGTTCGTATAGGAATTTCCCAATTTCAACAAATCTT 801  
QY 802 CCAAGAAATCCATCCATGGCAGATTTATGAAGCAGGATCTTTACTTTTGGGACATGGATA 861  
Db 802 CCAAGAAATCCATCCATGGCAGATTTATGAAGCAGGATCTTTACTTTTGGGACATGGATA 861  
QY 862 TACTCAGTTTAAAGGAGCAGCTTGCAGAGCTGGATTTTATGCTTTAGGTGAAGGTGAT 921  
Db 862 TACTCAGTTTAAAGGAGCAGCTTGCAGAGCTGGATTTTATGCTTTAGGTGAAGGTGAT 921  
QY 922 AAAGTAAAGTCTTCTCACTGTGGAGGAGGCTAACTGATTGGAAGCCAGTGAAGACCT 981  
Db 922 AAAGTAAAGTCTTCTCACTGTGGAGGAGGCTAACTGATTGGAAGCCAGTGAAGACCT 981  
QY 982 TGGGAACAACATGCTAAATGATATCCAGGGTGCAAAATATCTGTTAGAACAGAGGACAA 1041  
Db 982 TGGGAACAACATGCTAAATGATATCCAGGGTGCAAAATATCTGTTAGAACAGAGGACAA 1041

Qy 1042 GAATATATAACAATATTTACTTAACTTCACTTGAGGAGTGTCTGGTAAGAACTACT 1101  
Db 1042 GAATATATAACAATATTTACTTAACTTCACTTGAGGAGTGTCTGGTAAGAACTACT 1101  
Qy 1102 GAGAAACACCATCACTAACTAGAGAAATTTGATGATACCATCTTCCAAAATCCCTATGGTA 1161  
Db 1102 GAGAAACACCATCACTAACTAGAGAAATTTGATGATACCATCTTCCAAAATCCCTATGGTA 1161  
Qy 1162 CAAGAAGCTATACGAATGGGTTTCAGTTTCAAGGACATTAAGAAATTAATGGAGGAAAA 1221  
Db 1162 CAAGAAGCTATACGAATGGGTTTCAGTTTCAAGGACATTAAGAAATTAATGGAGGAAAA 1221  
Qy 1222 ATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTTCTGGTTGCAGATCTAGTGAAT 1281  
Db 1222 ATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTTCTGGTTGCAGATCTAGTGAAT 1281  
Qy 1282 GCTCAGAAGACAGTATCCAGAGAGTCAAGTCAGATCTTATACAGAAAGATTAAGT 1341  
Db 1282 GCTCAGAAGACAGTATCCAGAGAGTCAAGTCAGATCTTATACAGAAAGATTAAGT 1341  
Qy 1342 ACTGAAGAGCAGCTAAGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGA 1401  
Db 1342 ACTGAAGAGCAGCTAAGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGA 1401  
Qy 1402 AATATGCTATCGTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGCTGTA 1461  
Db 1402 AATATGCTATCGTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGCTGTA 1461  
Qy 1462 GCAGTTGACAGTGTCCCATGTGTACACAGTCACTTCAAGCAAAAATTTTATG 1521  
Db 1462 GCAGTTGACAGTGTCCCATGTGTACACAGTCACTTCAAGCAAAAATTTTATG 1521  
Qy 1522 TCTTAATCTAATCTATAGTAGGATGTTATGTTCTTATATCCCGATTGAATGTT 1581  
Db 1522 TCTTAATCTAATCTATAGTAGGATGTTATGTTCTTATATCCCGATTGAATGTT 1581  
Qy 1582 GATGTGAACCTTAAAGTAACTAGGATTAATCCATAGCACTTGTACCAAGTAGG 1641  
Db 1582 GATGTGAACCTTAAAGTAACTAGGATTAATCCATAGCACTTGTACCAAGTAGG 1641  
Qy 1642 AAAAAAATGTACATGGCAGTGTGTAGTGGCAATATAATCTTTGAATTTCTGATTTT 1701  
Db 1642 AAAAAAATGTACATGGCAGTGTGTAGTGGCAATATAATCTTTGAATTTCTGATTTT 1701  
Qy 1702 TCAGGTATATAGTGTATATCCATTTTCTTCTGTTTATTAATGAAACCATAGACTA 1761  
Db 1702 TCAGGTATATAGTGTATATCCATTTTCTTCTGTTTATTAATGAAACCATAGACTA 1761  
Qy 1762 AGAATAAGAAGCATCATATACTAATACTGAACACAATGTGTTATCTATAGTATATCTGATTTAA 1821  
Db 1762 AGAATAAGAAGCATCATATACTAATACTGAACACAATGTGTTATCTATAGTATATCTGATTTAA 1821  
Qy 1822 TTTCTAAGTGTAAAGTAAATTAATCATCTGGATTTTATTTCTTTTCAGATAGGCTTAACA 1881  
Db 1822 TTTCTAAGTGTAAAGTAAATTAATCATCTGGATTTTATTTCTTTTCAGATAGGCTTAACA 1881  
Qy 1882 AATGAGCTTTCTGTATATAATGTGGAGATTAGAGTTAATCTCCCAATCACATAATTT 1941  
Db 1882 AATGAGCTTTCTGTATATAATGTGGAGATTAGAGTTAATCTCCCAATCACATAATTT 1941  
Qy 1942 GTTTTGTGAAAAAGGAATAAATTTGTTCCATGCTGGTGGAAAGATAGAGATTTGTTTTTA 2001  
Db 1942 GTTTTGTGAAAAAGGAATAAATTTGTTCCATGCTGGTGGAAAGATAGAGATTTGTTTTTA 2001  
Qy 2002 GAGGTGTGTTGTTGTTTGGATTTCTGTCATTTCTT 2041  
Db 2002 GAGGTGTGTTGTTGTTTGGATTTCTGTCATTTCTT 2041

RESULT 8  
AAZ48862  
ID, AAZ48862 standard; cDNA; 1659 BP.

XX AAZ48862;  
XX AC  
XX XX  
DT 24-MAR-2000 (first entry)  
XX  
DE Human XIAP coding sequence.  
XX  
KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta; transforming growth factor-beta activated kinase 1; monocytic migration; TAK1 binding protein 1; extracellular matrix protein production; cell growth inhibitor; beta-amyloid protein deposition; immunosuppression; Transforming growth factor-beta; ds.  
XX  
OS Homo sapiens.  
XX OS  
XX JPI1326328-A.  
XX  
PD 26-NOV-1999.  
XX  
PF 13-MAY-1998; 98JP-0130378.  
XX  
PR 13-MAY-1998; 98JP-0130378.  
XX  
PA (MATSU) MATSUMOTO K.  
XX  
XX WPI; 2000-078337/07.  
DR DR  
DR P-PSDB; AAY59451.  
XX  
PT Screening a substance which inhibits combination of the X-linked inhibitor of apoptosis protein -  
XX  
XX Disclosure; Page 28-30; 43pp; Japanese.  
XX  
CC This sequence encodes the human XIAP protein.  
CC The invention relates to a method for screening a substance inhibiting the formation of a complex between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein (XIAP), transforming growth factor-beta activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be tested are contacted with each other and then the presence or formation of a complex between XIAP and TAB1 is detected. The substance can be used as a drug for extracellular matrix protein production enhancement, cell growth inhibition, monocytic migration, physiologically active substance induction, immunosuppression, and beta-amyloid protein deposition. A substance inhibiting the formation of a complex between TAB1 and XIAP as well as between XIAP and TGF-beta (transforming growth factor-beta) type CC I and/or type II receptor is useful as a drug.  
XX  
XX Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;  
S  
Query Match 29.8%; Score 1560; DB 21; Length 1659;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GAAAGGTGGACAGTCTCTATTTTCAAGAGAGATGACTTTTAAAGGATCT 60  
Db 49 GAAAGGTGGACAGTCTCTATTTTCAAGAGAGATGACTTTTAAAGGATCT 108  
Qy 61 AAAACTTGTGTACCTGCGACATCAATAAGCAAGAAGATTTGTAGAAGAGTTTAATAGA 120  
Db 109 AAAACTTGTGTACCTGCGACATCAATAAGCAAGAAGATTTGTAGAAGAGTTTAATAGA 168  
Qy 121 TTAATAAATTTTGTCTAATTTTCCAAAGTGTAGTCTCTGTTTCAGCATCAACACTGGCAGCA 180  
Db 169 TTAATAAATTTTGTCTAATTTTCCAAAGTGTAGTCTCTGTTTCAGCATCAACACTGGCAGCA 228  
Qy 181 GCAGGTTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGTTGTCATGCAGCT 240  
Db 229 GCAGGTTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGTTGTCATGCAGCT 288  
Qy 241 GTAGATAGTGGCAATATGGAGACTCAGCAGTTGAGAGACAGAGAAAGTATCCCAAT 300  
Db 289 GTAGATAGTGGCAATATGGAGACTCAGCAGTTGAGAGACAGAGAAAGTATCCCAAT 348

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QY 301 TGCAGATTATCAACGGCTTTTATCTGTGAAATAGTGCCACGAGCTCAAAATTCCTGGT 360
DB 349 TGCAGATTATCAACGGCTTTTATCTGTGAAATAGTGCCACGAGCTCAAAATTCCTGGT 408
QY 361 ATCCAGAAATGGTCAGTACAAAGTTGAAACTATCTCGGGAAGCAGAGATCATTTTGGCTT 420
DB 409 ATCCAGAAATGGTCAGTACAAAGTTGAAACTATCTCGGGAAGCAGAGATCATTTTGGCTT 468
QY 421 GACAGGCCATCTCAGACACATGACAGACTATCTTTTGTGAGAACTGGCAGGTTGTAGATATA 480
DB 469 GACAGGCCATCTCAGACACATGACAGACTATCTTTTGTGAGAACTGGCAGGTTGTAGATATA 528
QY 481 TCAGACACCATATACCCGAGGAACCTCGCATATATAGTGAAGAAGCTAGATATAAGTCC 540
DB 529 TCAGACACCATATACCCGAGGAACCTCGCATATATAGTGAAGAAGCTAGATATAAGTCC 588
QY 541 TTTTCAGAACTGGCCAGACATATGCTACCTAACCCCAAGAGAGTTAGCAAGTGTGACATC 600
DB 589 TTTTCAGAACTGGCCAGACATATGCTACCTAACCCCAAGAGAGTTAGCAAGTGTGACATC 648
QY 601 TACTACACAGGTATTGGTGACCAAGTGCACTGCTTTTGTGTGAGAACTGAAAAAT 660
DB 649 TACTACACAGGTATTGGTGACCAAGTGCACTGCTTTTGTGTGAGAACTGAAAAAT 708
QY 661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTCTTAATTCCTTCTTT 720
DB 709 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTCTTAATTCCTTCTTT 768
QY 721 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTGATAGGAAT 780
DB 769 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTGATAGGAAT 828
QY 781 TTCCCAAAATCAAAATCTTCCAGAAATCCATCCATGCGAGATTATGAAGCACGGATC 840
DB 829 TTCCCAAAATCAAAATCTTCCAGAAATCCATCCATGCGAGATTATGAAGCACGGATC 888
QY 841 TTTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGSAGCAGCTTCAAGAGCTGGATTT 900
DB 889 TTTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGSAGCAGCTTCAAGAGCTGGATTT 948
QY 901 TATGCTTTTAGTGAAGTGAATGAATGAAGTGTCTTCACTGTGGAGGAGGCTTAACGTGAT 960
DB 949 TATGCTTTTAGTGAAGTGAATGAATGAAGTGTCTTCACTGTGGAGGAGGCTTAACGTGAT 1008
QY 961 TGGAAAGCCAGTCAAGACCTTGGGAACACATCTGTAATGTAATGTAATCCAGGTCGCAATAT 1020
DB 1009 TGGAAAGCCAGTCAAGACCTTGGGAACACATCTGTAATGTAATGTAATCCAGGTCGCAATAT 1068
QY 1021 CTGTTAGAAGAGGAGGACAAAGATATATAAACAATATTCATTTAACTCAATTCACCTTGAG 1080
DB 1069 CTGTTAGAAGAGGAGGACAAAGATATATAAACAATATTCATTTAACTCAATTCACCTTGAG 1128
QY 1081 GAGTGTCTGTAGAACTACTGAGAAACACCAATCACTAATCAAGAAATTTGATGATACC 1140
DB 1129 GAGTGTCTGTAGAACTACTGAGAAACACCAATCACTAATCAAGAAATTTGATGATACC 1188
QY 1141 ATCTTCAAAATCTATGGTACAAAGCTATACGAATGGGTTTCAGTTTCAAGGACATTT 1200
DB 1189 ATCTTCAAAATCTATGGTACAAAGCTATACGAATGGGTTTCAGTTTCAAGGACATTT 1248
QY 1201 AAGAAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
DB 1249 AAGAAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1308
QY 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAAGCT 1320
DB 1309 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAAGCT 1368
QY 1321 TCATTCAGAAAGACAGATATGCTAGTGAAGACAGCTAAGGCGCTGCAAGAGGAGGAGCTTT 1380
DB 1369 TCATTCAGAAAGACAGATATGCTAGTGAAGACAGCTAAGGCGCTGCAAGAGGAGGAGCTTT 1428
QY 1381 TGCAAAATCTGTATGGATAGAAATATTTGCTATCGTTTTTTTCTTCTTGTGGACATCTAGTC 1440
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DB 1429 TCGAAAATCTGTATGGATAGAAAATATTCGTATCGTTTTTCTTCTTGTGGACATCTAGTC 1488
QY 1441 ACTTGTAAACAATGCTGTGAAGCAGTTGACAAGTGTCCCATGTGCTTACACAGTCATTACT 1500
DB 1489 ACTTGTAAACAATGCTGTGAAGCAGTTGACAAGTGTCCCATGTGCTTACACAGTCATTACT 1548
QY 1501 TTCAAGCAAAAAATTTTATGTCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCT 1560
DB 1549 TTCAAGCAAAAAATTTTATGTCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCT 1608
QY 1561 TATTACCCCTGATTGAATGTGTGATGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1611
DB 1609 TATTACCCCTGATTGAATGTGTGATGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1659

RESULT 9
AAK89469
ID AAK89469 standard; DNA; 469 BP.
XX
AC AAK89469;
XX
DT 05-NOV-2001 (first entry)
XX
Human digestive system antigen genomic sequence SEQ ID NO: 3045.
DE
KW Human: digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX
OS Homo sapiens.
XX
PN WO200155314-A2.
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01324.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226861.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
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Db 301 TTTCTAAGTCTAAGTGAATTAATCATCTCGATTTTATTTCTTTTTCAGATAGGCTTAAACA 360  
QY 1882 AATGGAGCTTTCGTATATAAATGTGGAGATTAGAGTTAATCTCCCAATCACATAATTT 1941  
Db 361 AATGGAGCTTTCGTATATAAATGTGGAGATTAGAGTTAATCTCCCAATCACATAATTT 420  
QY 1942 GTTTTCTGTGAAGAAAGATAAATCTTCCATGCTGGTGGAAAGATAGA 1990  
Db 421 GTTTTCTGTGAAGAAAGATAAATCTTCCATGCTGGTGGAAAGATAGA 469  
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ABA43584/C  
ID ABA43584 standard; DNA; 489 BP.  
XX  
AC ABA43584;  
XX  
XX  
DT 01-FEB-2002 (first entry)  
XX  
DE Human breast cell single exon nucleic acid probe #2279.  
XX  
XX Human; microarray; single exon probe; gene expression; breast;  
KW disease; cancer; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200157271-A2.  
PN  
XX  
PD 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US00662.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-496933/54.  
DR  
XX  
XX New spatially-addressable set of single exon nucleic acid probes,  
PT useful for measuring gene expression in sample derived from human  
PT breast, comprises number of single exon nucleic acid probes -  
XX  
XX  
PS Claim 1; SEQ ID NO 2279; 327pp + sequence listing; English.  
XX  
XX The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human breast and BT 474 cells. The method involves contacting  
CC the probes with a collection of detectably labelled nucleic acids  
CC derived from mRNA of human breast, and then measuring the label  
CC bound to each probe of the microarray. The probes are useful for  
CC verifying the expression of regions of genomic DNA predicted to  
CC encode proteins. They are useful for gene discovery, and for  
CC determining predisposition and/or prognosing breast disease. Gene  
CC expression analysis is useful for assessing the toxicity of chemical  
CC agents on cells. The microarray of this invention presents a far greater  
CC diversity of probes for measuring gene expression, with far less bias  
CC than expressed sequence tag microarrays. The method is suitable for  
CC rapid production of functional information from genomic sequence. The  
CC present sequence is a single exon nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 489 BP; 175 A; 90 C; 73 G; 151 T; 0 other;  
Query Match 8.9%; Score 466; DB 22; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.7e-161;  
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1332 AGAGATTAGTACTGAAGAGCAGCTAAGGCGCCTGCAAGAGAGGAAGCTTTGCAAAATCTG 1391  
Db 466 AGAGATTAGTACTGAAGAGCAGCTAAGGCGCCTGCAAGAGAGGAAGCTTTGCAAAATCTG 407  
QY 1392 TATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACA 1451  
Db 406 TATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACA 347  
QY 1452 ATGTGCTGAAGCAGTTGACAAAGTGTCCCATGTCTACACAGTCATTACTTTTCRAGCAAAA 1511  
Db 346 ATGTGCTGAAGCAGTTGACAAAGTGTCCCATGTCTACACAGTCATTACTTTTCRAGCAAAA 287  
QY 1512 AATTTTATGTCCTTAATCTAATCTATAGTAGGCATGTTATGTGTCTTTATTACCCCTGA 1571  
Db 286 AATTTTATGTCCTTAATCTAATCTATAGTAGGCATGTTATGTGTCTTTATTACCCCTGA 227  
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QY 1632 ACCAAGTAGGAAAAAATGTACATGCGCAGTGTTTAGTTGGCAATATAATCTTTGAATT 1691  
Db 166 ACCAAGTAGGAAAAAATGTACATGCGCAGTGTTTAGTTGGCAATATAATCTTTGAATT 107  
QY 1692 TCTTGTATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTATTATTAATGAAA 1751  
Db 106 TCTTGTATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTATTATTAATGAAA 47  
QY 1752 CCATAGACTAAGAAATAGAAGCATCATACTATATAACTGAACACAATG 1797  
Db 46 CCATAGACTAAGAAATAGAAGCATCATACTATATAACTGAACACAATG 1  
RESULT 11  
AAI12335/C  
ID AAI12335 standard; DNA; 489 BP.  
XX  
XX  
AC AAI12335;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Probe #2268 for gene expression analysis in human cervical cell sample.  
XX  
DE Probe; human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200157278-A2.  
PN  
XX  
PD 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US00670.  
XX  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI



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QY 1752 CCATAGACTAAGATAAGAGCATCATATACCTAATGACACAAATG 1797
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Db 46 CCATAGACTAAGATAAGAGCATCATATACCTAATGACACAAATG 1
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ID AAH33140 standard; cDNA; 417 BP.
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AC AAH33140;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:196.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome X; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG73709.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 1; Page 2344; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 417 BP; 118 A; 61 C; 65 G; 172 T; 1 other;

Query Match 6.9%; Score 359; DB 22; Length 417;
Best Local Similarity 99.9%; Pred. No. 3.3e-122;
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||||
Db 1 TTTCACCTTCTACTTTTTCATTTTGTCTGCTCGAATTTTATAAGTATGATTACTT 60
|||||

QY 2410 TTGTAATCAGAAATTTTGAAGATATTTTGTCTGATTTTAAAGGCTTAGGCATGTTCAAACG 2469
|||||
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Db 61 TTGTAATCAGAAATTTTGAAGATATTTTGTCTGATTTTAAAGGCTTAGGCATGTTCAAACG 120
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QY 2530 ACCTTTTGTGCGCAATGTGAAATGTAATGATTTTATGTTTTCCTGCTTTTGTGGATGA 2589
|||||
Db 181 ACCTTTTGTGCGCAATGTGAAATGTAATGATTTTATGTTTTCCTGCTTTTGTGGATGA 240
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QY 2590 AAAATATTTCTGAGTGGTAGTTTTTGCACAGGTAGACCATGCTTATCTGTTCAAAAT 2649
|||||
Db 241 AAAATATTTCTGAGTGGTAGTTTTTGCACAGGTAGACCATGCTTATCTGTTCAAAAT 300
|||||
QY 2650 AAGTATTTCTGATTTTGTAAATGAAATATATAATATGTCACAGATCTTCCAAATTAATTA 2709
|||||
Db 301 AAGTATTTCTGATTTTGTAAATGAAATATATAATATGTCACAGATCTTCCAAATTAATTA 360
|||||
QY 2710 GTAAGGATTCATCCTTAATCCTGCTAGTTTAAAGCCTGCGCTAAGTCACTT 2759
|||||
Db 361 GTAAGGATTCATCCTTAATCCTGCTAGTTTAAAGCCTGCGCTAAGTCACTT 410
|||||

RESULT 14
AAC25231
ID AAC25231 standard; cDNA; 315 BP.
XX
AC AAC25231;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 29306.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 29306; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
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OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 15338381 residues

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Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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5: /cgn2.6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2.6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5232	100.0	5232	US-09-212-971-3	Sequence 3, Appli
2	5232	100.0	5232	US-08-800-929A-3	Sequence 3, Appli
3	5232	100.0	5232	US-09-617-053A-3	Sequence 3, Appli
4	1990	38.0	2540	US-08-511-485-3	Sequence 3, Appli
5	1990	38.0	2540	US-09-392-580-1	Sequence 1, Appli
6	1588	30.4	1588	US-09-239-867-3	Sequence 3, Appli
7	103	2.0	40328	US-08-742-185-102	Sequence 102, App
8	103	2.0	43795	US-08-742-185-101	Sequence 101, App
9	83	1.6	152331	US-09-128-155-16	Sequence 16, Appli
10	81	1.5	3494	US-09-334-601-5	Sequence 5, Appli
11	74	1.4	19736	US-09-740-035-3	Sequence 3, Appli
12	70	1.3	11298	US-07-869-933-31	Sequence 31, Appli
13	70	1.3	11298	US-08-201-879A-2	Sequence 2, Appli
14	70	1.3	11298	US-09-103-663-31	Sequence 31, Appli
15	69	1.3	14581	US-08-520-373D-4	Sequence 4, Appli
16	69	1.3	22481	US-08-367-841A-43	Sequence 43, Appli
17	69	1.3	22481	PCT-US95-07201-43	Sequence 43, Appli
18	69	1.3	22484	US-09-875-223-2	Sequence 2, Appli
19	69	1.3	16998	US-09-676-610B-24	Sequence 24, Appli
20	67	1.3	859	US-09-535-008-58	Sequence 58, Appli
21	67	1.3	36651	US-09-738-894A-3	Sequence 3, Appli
22	67	1.3	70000	US-09-851-896-3	Sequence 3, Appli
23	66	1.3	534	US-08-599-252-101	Sequence 101, App
24	66	1.3	534	PCT-US96-06352-101	Sequence 101, App
25	66	1.3	534	PCT-US96-06583-101	Sequence 101, App
26	66	1.3	956	US-09-641-638-41	Sequence 41, Appli
27	66	1.3	1712	US-09-058-389A-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1

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; Sequence 3, Application US/09212971B  
; Patent No. 6107041  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: MacKenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 07891/009002  
; CURRENT APPLICATION NUMBER: US/09/212,971B  
; CURRENT FILING DATE: 1998-12-16  
; EARLIER APPLICATION NUMBER: 60/017,354  
; EARLIER FILING DATE: 1996-04-26  
; EARLIER APPLICATION NUMBER: 60/030,590  
; EARLIER FILING DATE: 1996-11-14  
; EARLIER APPLICATION NUMBER: 08/800,929  
; EARLIER FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 5232  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (4623)...(4623)  
; OTHER INFORMATION: n can be any nucleotide  
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; NAME/KEY: variation  
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US-09-212-971-3

Query Match 100.0%; Score 5232; DB 3; Length 5232;

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Matches 5232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT 60

|||||

Qy 61 AAAACTTGTGTACCTGCGAGACATCAATAAGGAAGAAGATTTGTAGAGAGTTTAATAGA 120

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Db 61 AAAACTTGTGTACCTGCGAGACATCAATAAGGAAGAAGATTTGTAGAGAGTTTAATAGA 120

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Db 121 TTAATAAATCTTTGCTAAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCAACACTGSCACGA 180  
Qy 181 GCAGGTTTCTTTATACGTGGTGAAGGAGATACCGTGCCTGCTTTAGTTGTCAGTCAGCT 240  
Db 181 GCAGGTTTCTTTATACGTGGTGAAGGAGATACCGTGCCTGCTTTAGTTGTCAGTCAGCT 240  
Qy 241 GTAGATAGTGCATATGGAGACTCAGCAGCTTGAAGACACAGAGAAAGTATCCCAAT 300  
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Qy 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGCACGAGTCTACAAATTCGCT 360  
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGCACGAGTCTACAAATTCGCT 360  
Qy 361 ATCCAGAAATGTCAGTACAAAGTGAAGTGAAGTATCTGCGGAGCAGAGATCAATTTGCCPTA 420  
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Db 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGTACATGSCAGTGTGTTAGTTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTGATTTTTCAGGCTATTAGCTGTATTATCCCATTTTTTTTACTGTTA 1740  
Db 1681 ATCTTTGAATTTCTGATTTTTCAGGCTATTAGCTGTATTATCCCATTTTTTTTACTGTTA 1740  
Qy 1741 TTTAATTTGAAACCATFAGACTAAGATAAGAAAGCATCATACTATACTGAACACAATGTGT 1800  
Db 1741 TTTAATTTGAAACCATFAGACTAAGATAAGAAAGCATCATACTATACTGAACACAATGTGT 1800  
Qy 1801 ATTCATAGTATACGATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTTAT 1860  
Db 1801 ATTCATAGTATACGATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTTAT 1860  
Qy 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTCTATATAAATGCGAGATFAGAGTTA 1920  
Db 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTCTATATAAATGCGAGATFAGAGTTA 1920  
Qy 1921 ATCTCCCCAATCACATAATTTGTTGTGTAAGAAAGGAATAAATGTTCCATGCTGGT 1980  
Db 1921 ATCTCCCCAATCACATAATTTGTTGTGTAAGAAAGGAATAAATGTTCCATGCTGGT 1980  
Qy 1981 GAAAGATAGAGATTTCTTTTACAGGTTGGTCTGTTCTTTAGGATCTGTCATTTCT 2040  
Db 1981 GAAAGATAGAGATTTCTTTTACAGGTTGGTCTGTTCTTTAGGATCTGTCATTTCT 2040  
Qy 2041 TTTAAAGTTATAACACACGCTACTTGTGCGAATTTATTTTTTAAAGTGATTTGCCATTTTG 2100  
Db 2041 TTTAAAGTTATAACACACGCTACTTGTGCGAATTTATTTTTTAAAGTGATTTGCCATTTTG 2100  
Qy 2101 AAAGGATTTAATGATAGATFATCGAGCCAACTACTGACATGGAAGATGCA 2160  
Db 2101 AAAGGATTTAATGATAGATFATCGAGCCAACTACTGACATGGAAGATGCA 2160  
Qy 2161 AAGATATCTTAAGCTAAATGCAAGTGCAGCAACACATGATGATAGTCTGAGCCAGATCA 2220  
Db 2161 AAGATATCTTAAGCTAAATGCAAGTGCAGCAACACATGATGATAGTCTGAGCCAGATCA 2220  
Qy 2221 AAGTATGATGTTTTTAAATATGATAGCAACAAAGATTTGGAAGATATACACCAACTG 2280  
Db 2221 AAGTATGATGTTTTTAAATATGATAGCAACAAAGATTTGGAAGATATACACCAACTG 2280  
Qy 2281 TTAATGTTGTTCTCTTTCCGGGAGGGGGGATTTGGGGAGGGGCCCCAGAGGGTTTTTA 2340

[illegible]

Db	3361	GC	AAATATATTTTATTTATTTAAATTTCTTTTGGAGATGGAGTCTTGTTGTCACCCAGG	34220
Qy	3421	CT	GGAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCCCTTCTGGGTTTCAAGCGAT	3480
Db	3421	CT	GGAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCCCTTCTGGGTTTCAAGCGAT	3480
Qy	3481	TCT	CGTGCCCTCAGCTTCTCTGAGTAGTGTGAATTTACAGGCAGGTGCCACCATGCCCGACTA	3540
Db	3481	TCT	CGTGCCCTCAGCTTCTCTGAGTAGTGTGAATTTACAGGCAGGTGCCACCATGCCCGACTA	3540
Qy	3541	AT	TTTTTTTTTATTTTTAGTAGAGCGGGTTTCCACCATGTGSCCAGGCTGGTGTATCAAAC	3600
Db	3541	AT	TTTTTTTTTATTTTTAGTAGAGCGGGTTTCCACCATGTGSCCAGGCTGGTGTATCAAAC	3600
Qy	3601	TC	CTGACCTCAAGAGATCCACCTCGCCTTCGCCCTCCCAAAGTGCCTGGGATTTACAGGCTTGA	3660
Db	3601	TC	CTGACCTCAAGAGATCCACCTCGCCTTCGCCCTCCCAAAGTGCCTGGGATTTACAGGCTTGA	3660
Qy	3661	GCC	ACCAGCCCGCGCTAAACAATTTGCAAAATTTAAATGAGAGTTTTTAAAAATTTAAATAATG	3720
Db	3661	GCC	ACCAGCCCGCGCTAAACAATTTGCAAAATTTAAATGAGAGTTTTTAAAAATTTAAATAATG	3720
Qy	3721	ACT	GCCCTGTTTCTGTTTGTAGTAGTGTAAATCCCTCAGTCTTTCACCTTTCGCATGCTGCGC	3780
Db	3721	ACT	GCCCTGTTTCTGTTTGTAGTAGTGTAAATCCCTCAGTCTTTCACCTTTCGCATGCTGCGC	3780
Qy	3781	ACT	TAGTTTGGTTATATAGTCAATTAACCTGAAATTTGGTCTGTATAGTCTAGACTTTAAAT	3840
Db	3781	ACT	TAGTTTGGTTATATAGTCAATTAACCTGAAATTTGGTCTGTATAGTCTAGACTTTAAAT	3840
Qy	3841	TT	AAAGTTTTCTACAAGGGGAAAGAGTGTAAAAATTTTAAAAATATGTTTCCAGGACA	3900
Db	3841	TT	AAAGTTTTCTACAAGGGGAAAGAGTGTAAAAATTTTAAAAATATGTTTCCAGGACA	3900
Qy	3901	CT	TCACTCCAGTCAGGTAGTGTCAATCTAGTTGTGTGCCCAAGGACTCAAGGACTG	3960
Db	3901	CT	TCACTCCAGTCAGGTAGTGTCAATCTAGTTGTGTGCCCAAGGACTCAAGGACTG	3960
Qy	3961	AA	TGTTTTTAACATAAGGCTTTTCTGTGTCGCGGAGCCGACATTCATTAATAATCTCTCTA	4020
Db	3961	AA	TGTTTTTAACATAAGGCTTTTCTGTGTCGCGGAGCCGACATTCATTAATAATCTCTCTA	4020
Qy	4021	AA	CTTGATGTTTTAGAGTTAAGCAAGACTTTTTTTCTCCTCTCCATGAGTTGTGAAAT	4080
Db	4021	AA	CTTGATGTTTTAGAGTTAAGCAAGACTTTTTTTCTCCTCTCCATGAGTTGTGAAAT	4080
Qy	4081	TT	AATGCAACGCTGATGCTGCTACAGAGTTATTTTAAAGAAATGTTTAAAGAAATGCTGT	4140
Db	4081	TT	AATGCAACGCTGATGCTGCTACAGAGTTATTTTAAAGAAATGTTTAAAGAAATGCTGT	4140
Qy	4141	TG	CTTCAGGTTCTTAAAAATCACTCAGCACTCCAACTTCTAATCAAAATTTTTTGGAGACTTA	4200
Db	4141	TG	CTTCAGGTTCTTAAAAATCACTCAGCACTCCAACTTCTAATCAAAATTTTTTGGAGACTTA	4200
Qy	4201	AC	AGCATTTGTCGTGTTTTGAACATATAAAAGACCGGATCTTTTCCATCTAATTCGCA	4260
Db	4201	AC	AGCATTTGTCGTGTTTTGAACATATAAAAGACCGGATCTTTTCCATCTAATTCGCA	4260
Qy	4261	AAA	ATTGATCATTTGCAAAAGTCAAAACATATAGCCATATCCAAATCTTTTCCCTCCCAA	4320
Db	4261	AAA	ATTGATCATTTGCAAAAGTCAAAACATATAGCCATATCCAAATCTTTTCCCTCCCAA	4320
Qy	4321	GAG	TCTCAGTCTACATGTAGACTATTTCTTTCTGTATAAGTTTCACCTCTAGGATTT	4380
Db	4321	GAG	TCTCAGTCTACATGTAGACTATTTCTTTCTGTATAAGTTTCACCTCTAGGATTT	4380
Qy	4381	CA	AGTCACCACCTATTTTACATTTTAGTCAATGCAAAAGATTTCAAGTAGTTTGGCAATAAGT	4440
Db	4381	CA	AGTCACCACCTATTTTACATTTTAGTCAATGCAAAAGATTTCAAGTAGTTTGGCAATAAGT	4440
Qy	4441	ACT	ATCTTTATTTTGAATAAATTTAGTCTGCTGATCAAAAGCATGTGCTTAATTTTGTAG	4500
Db	4441	ACT	ATCTTTATTTTGAATAAATTTAGTCTGCTGATCAAAAGCATGTGCTTAATTTTGTAG	4500

Qy 4501 AACTGGTTTATAGCAATTAACAACAACTAAATCCAGTTAAATTAATTAATAGCTTTATATTGCC 4560  
Db 4501 AACTGGTTTATAGCAATTAACAACAACTAAATCCAGTTAAATTAATTAATAGCTTTATATTGCC 4560  
Qy 4561 TTTCCTGCTACATTTGGTTTTTCCCTCCCTGCTCCCTTTGATTAAGGGCTAAGGTAGGTAAG 4620  
Db 4561 TTTCCTGCTACATTTGGTTTTTCCCTCCCTGCTCCCTTTGATTAAGGGCTAAGGTAGGTAAG 4620  
Qy 4621 ANNGGCTGAGTACGTATATATGTCATTTGGCCCTGCTGCTATTAATATATATTTGTTAT 4680  
Db 4621 ANNGGCTGAGTACGTATATATGTCATTTGGCCCTGCTGCTATTAATATATATTTGTTAT 4680  
Qy 4681 TTTTCTGTTAT 4740  
Db 4681 TTTTCTGTTAT 4740  
Qy 4741 AAAATTTGTTAT 4800  
Db 4741 AAAATTTGTTAT 4800  
Qy 4801 TACCCTTTAAACCCGAATCATTTGTTTATTTCCCTGATTAACAGGTGTTGAATGGGAAA 4860  
Db 4801 TACCCTTTAAACCCGAATCATTTGTTTATTTCCCTGATTAACAGGTGTTGAATGGGAAA 4860  
Qy 4861 GGGGCTAGTATATACAGTAT 4920  
Db 4861 GGGGCTAGTATATACAGTAT 4920  
Qy 4921 ATGAATTAATAGGGCTGGGCTAGTGGCTACGCCCTGTAATCCACACACTTTGGGAGG 4980  
Db 4921 ATGAATTAATAGGGCTGGGCTAGTGGCTACGCCCTGTAATCCACACACTTTGGGAGG 4980  
Qy 4981 CTGAGGAGGTGGATCAGAGGTACAGGATCGAGACCATCTGGCTAACACGTTGAAC 5040  
Db 4981 CTGAGGAGGTGGATCAGAGGTACAGGATCGAGACCATCTGGCTAACACGTTGAAC 5040  
Qy 5041 CCCGCTCTACTAAAAACAGAAAAATTAGCCGGGCTGGTGGCGGCGCCCTGTAGTCCCA 5100  
Db 5041 CCCGCTCTACTAAAAACAGAAAAATTAGCCGGGCTGGTGGCGGCGCCCTGTAGTCCCA 5100  
Qy 5101 GCTACTCGGGAGGCTGAGCGAGGAGAAATGGTGTGNAACCCGGGAGGACAGCTTGCAGTGA 5160  
Db 5101 GCTACTCGGGAGGCTGAGCGAGGAGAAATGGTGTGNAACCCGGGAGGACAGCTTGCAGTGA 5160  
Qy 5161 GCCGAGATCTCGCCACTGCACCTCCAGCCTGGGCAACAGCAAGACTCTGTCTCAAAAAA 5220  
Db 5161 GCCGAGATCTCGCCACTGCACCTCCAGCCTGGGCAACAGCAAGACTCTGTCTCAAAAAA 5220  
Qy 5221 AAAAAAAG 5232  
Db 5221 AAAAAAAG 5232

RESULT 2  
US-08-800-929A-3  
; Sequence 3, Application US/08800929A  
; Patent No. 6133437  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF  
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston

STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,929A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/030,590  
FILING DATE: 14-NOV-1996  
APPLICATION NUMBER: 60/017,354  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bieker-Brady, Kristina  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 07891/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: Other  
LOCATION: 1...5232  
OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.  
US-08-800-929A-3

Query Match 100.0%; Score 5232; DB 3; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAAGGTGGCAAGTCTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Db 1 GAAAGGTGGCAAGTCTCTATTTTCAAGAGAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Qy 61 AAAACTTGTGTACCTGCAGACATCAATGAAGAGAGAAATTTGTAGAAGAGTTTAATAGA 120  
Db 61 AAAACTTGTGTACCTGCAGACATCAATGAAGAGAGAAATTTGTAGAAGAGTTTAATAGA 120  
Qy 121 TAAAAACTTTTGTCTAATTTTCCAAAGTGTAGTCTCTGTTTCAGCATCAACACTGGCAGGA 180  
Db 121 TAAAAACTTTTGTCTAATTTTCCAAAGTGTAGTCTCTGTTTCAGCATCAACACTGGCAGGA 180  
Qy 181 GCAGGGTTTCTTATACCTGGAAGAGATACCGTGCAGTGTCTTTAGTTGTCTAGTCA 240  
Db 181 GCAGGGTTTCTTATACCTGGAAGAGATACCGTGCAGTGTCTTTAGTTGTCTAGTCA 240  
Qy 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTGTGAAGACACAGCAAGAGTATCCCAAT 300  
Db 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTGTGAAGACACAGCAAGAGTATCCCAAT 300  
Qy 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGCACGACAGTCTACAAATTTCTGT 360  
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTGCACGACAGTCTACAAATTTCTGT 360  
Qy 361 ATCCAGAAATGGTACAGTTTGAAGAGTGTGAAGAGAGATCATATTTTGCCTTA 420  
Db 361 ATCCAGAAATGGTACAGTTTGAAGAGTGTGAAGAGAGATCATATTTTGCCTTA 420  
Qy 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAAGAGTGGCAGGTTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAAGAGTGGCAGGTTGTAGATATA 480



QY 481 TCAGACACCATAATACCCGAGGAACCCCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC 540  
 Db 481 TCAGACACCATAATACCCGAGGAACCCCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC 540  
 QY 541 TTTTCAGAACTGGCCAGAGTATGCTCACTTAACCCCAAGAGAGTGTAGCAAGTGTGGAATC 600  
 Db 541 TTTTCAGAACTGGCCAGAGTATGCTCACTTAACCCCAAGAGAGTGTAGCAAGTGTGGAATC 600  
 QY 601 TACTACACAGGTATTTGGTGACCAAGTGCAGTCTTTTGTGTGCTGCAAAAT 660  
 Db 601 TACTACACAGGTATTTGGTGACCAAGTGCAGTCTTTTGTGTGCTGCAAAAT 660  
 QY 661 TGGGAACCTTTGTGATGCTGCTGGTGCAGAACACAGGCGACACTTTCCTAATTTGCTTCTTT 720  
 Db 661 TGGGAACCTTTGTGATGCTGCTGGTGCAGAACACAGGCGACACTTTCCTAATTTGCTTCTTT 720  
 QY 721 GTTTTGGCCGGGAATCTTAATATTCGAAGTGAATCTGATGCTGATAGGAAT 780  
 Db 721 GTTTTGGCCGGGAATCTTAATATTCGAAGTGAATCTGATGCTGATAGGAAT 780  
 QY 781 TTCCCAAATTCACAAATCTTCCAGAAATCCATCCATGCCAGATTAATGAAGCACCGATC 840  
 Db 781 TTCCCAAATTCACAAATCTTCCAGAAATCCATCCATGCCAGATTAATGAAGCACCGATC 840  
 QY 841 TTTTACTTTTGGGACATGGATATACTCAGTTTAAACAAGGAGCAGCTTGCAGAGCTGGATTT 900  
 Db 841 TTTTACTTTTGGGACATGGATATACTCAGTTTAAACAAGGAGCAGCTTGCAGAGCTGGATTT 900  
 QY 901 TATGCTTTAGTGAAGTGATTAAGTAAAGTCTTTCACGTGAGAGGAGGCTTAACGTAT 960  
 Db 901 TATGCTTTAGTGAAGTGATTAAGTAAAGTCTTTCACGTGAGAGGAGGCTTAACGTAT 960  
 QY 961 TGGAGCCCAAGTGAAGACCTTGGGACACATGCTTAATGCTATCAGGCTGCAATAT 1020  
 Db 961 TGGAGCCCAAGTGAAGACCTTGGGACACATGCTTAATGCTATCAGGCTGCAATAT 1020  
 QY 1021 CTGTTAGAACAGAGGAGACAAAGTATATAAACAATATTCATTAACTCACTTACCTTTGAG 1080  
 Db 1021 CTGTTAGAACAGAGGAGACAAAGTATATAAACAATATTCATTAACTCACTTACCTTTGAG 1080  
 QY 1081 GAGTGTCTGTAAGACTACTAGAAACACCATCACTAAGAGAAATGATGATACC 1140  
 Db 1081 GAGTGTCTGTAAGACTACTAGAAACACCATCACTAAGAGAAATGATGATACC 1140  
 QY 1141 ATCTTCCAAATCCTATGGTACAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATT 1200  
 Db 1141 ATCTTCCAAATCCTATGGTACAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATT 1200  
 QY 1201 AAGAAATATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT 1260  
 Db 1201 AAGAAATATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT 1260  
 QY 1261 CTGGTTGCAGACTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
 Db 1261 CTGGTTGCAGACTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
 QY 1321 TCATTACAGAAAGAGATTACTACTGAGAGCAGCTAAGGCGCTTGCAGAGGAGAGACTT 1380  
 Db 1321 TCATTACAGAAAGAGATTACTACTGAGAGCAGCTAAGGCGCTTGCAGAGGAGAGACTT 1380  
 QY 1381 TGCAAAATCTGATGGATAGAAATATTCGTATCTGTTTGTCTTGTGACATCTAGTC 1440  
 Db 1381 TGCAAAATCTGATGGATAGAAATATTCGTATCTGTTTGTCTTGTGACATCTAGTC 1440  
 QY 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCAATFACT 1500  
 Db 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCAATFACT 1500  
 QY 1501 TTCAAGCAAAAAATTTTATGCTCTTAATCTAATCTATAGTAGGCATGTTATGTTGTTCT 1560  
 Db 1501 TTCAAGCAAAAAATTTTATGCTCTTAATCTAATCTATAGTAGGCATGTTATGTTGTTCT 1560

QY 1561 TATTACCCCTGATTGAATGTGTGATGTGAACCTGACTTTTAAGTAATCAGGATTAATTCAT 1620  
 Db 1561 TATTACCCCTGATTGAATGTGTGATGTGAACCTGACTTTTAAGTAATCAGGATTAATTCAT 1620  
 QY 1621 TAGCATTTGCTACCAAGTAGAAAAAATGTACATGGCAGTGTTTAGTTTGGCAATATA 1680  
 Db 1621 TAGCATTTGCTACCAAGTAGAAAAAATGTACATGGCAGTGTTTAGTTTGGCAATATA 1680  
 QY 1681 ATCTTTTGAATTTCTTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTA 1740  
 Db 1681 ATCTTTTGAATTTCTTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTA 1740  
 QY 1741 TTTTAATTTGAACCATAGACTAAGAAATGAAGCATCATCTATAAATCAACACAATGTGT 1800  
 Db 1741 TTTTAATTTGAACCATAGACTAAGAAATGAAGCATCATCTATAAATCAACACAATGTGT 1800  
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 Db 1861 TCTTTTTCAGATAGGCTTAAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
 QY 1921 ATCTCCCAATCACATAAATTTGTTTGTGCAAAAAGAAATAAATTTGTCATCTGGTG 1980  
 Db 1921 ATCTCCCAATCACATAAATTTGTTTGTGCAAAAAGAAATAAATTTGTCATCTGGTG 1980  
 QY 1981 GAAAGATAGAGATTTTGTAGAGTTGGTTGTGTTTAGGATTTCTGTCCATTTTCT 2040  
 Db 1981 GAAAGATAGAGATTTTGTAGAGTTGGTTGTGTTTAGGATTTCTGTCCATTTTCT 2040  
 QY 2041 TTTTAAAGTTTAAACACGTACTTGTGCGAATTTATTTTTTAAAGTGATTTGCCATTTTGT 2100  
 Db 2041 TTTTAAAGTTTAAACACGTACTTGTGCGAATTTATTTTTTAAAGTGATTTGCCATTTTGT 2100  
 QY 2101 AAAGCGTATTTAATGATAGAAATCTATCGAGCCCAACATGTACTGACATGGAAGATGTCA 2160  
 Db 2101 AAAGCGTATTTAATGATAGAAATCTATCGAGCCCAACATGTACTGACATGGAAGATGTCA 2160  
 QY 2161 AAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACATGTATGTAGTCTGAGCCAGATCA 2220  
 Db 2161 AAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACATGTATGTAGTCTGAGCCAGATCA 2220  
 QY 2221 AAGTATCTATGTTTAAATGCAAGTGGCAAAACACATGTATGTAGTCTGAGCCAGATCA 2280  
 Db 2221 AAGTATCTATGTTTAAATGCAAGTGGCAAAACACATGTATGTAGTCTGAGCCAGATCA 2280  
 QY 2281 TTTAAATGTTTCTCTTCGGGAGGGGGGATTTGGGGAGGGGGCCAGAGGGGTTTTA 2340  
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 QY 2341 TAGGGGCTTTTCTACTTTCTACTTTTTCATTTTGTGCTGTTCGAATTTTTTATAAGTAT 2400  
 Db 2341 TAGGGGCTTTTCTACTTTTCTACTTTTTCATTTTGTGCTGTTCGAATTTTTTATAAGTAT 2400  
 QY 2401 GTATTACTTTGTAATCAGAAATTTTGAAGATTTTGTGATTTTAAAGCTTTAGGCAT 2460  
 Db 2401 GTATTACTTTGTAATCAGAAATTTTGAAGATTTTGTGATTTTAAAGCTTTAGGCAT 2460  
 QY 2461 GTTCAACGCGCTGCAAAACACTTATCAGTCAAGCTTTAGTTTCTAATCCAAAGAGCA 2520  
 Db 2461 GTTCAACGCGCTGCAAAACACTTATCAGTCAAGCTTTAGTTTCTAATCCAAAGAGCA 2520  
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 Db 2521 GGGCAGTTAACCTTTTGGTGCCCAATGTGAATCTAATGAATTTTATGTTTCTGCTT 2580  
 QY 2581 TGTGGATCAAAATATTTCTGAGTGGTATTTTTTGACAGGTAGACCATGCTTATCTTG 2640  
 Db 2581 TGTGGATCAAAATATTTCTGAGTGGTATTTTTTGACAGGTAGACCATGCTTATCTTG 2640  
 QY 2641 TTTCAAAAATAGTATTTCTGATTTTGTAAATGAAATATAAATATATGCTCAGATCTTCC 2700

Db	2641	 TTTTCAAAATAAGTATTCTTGATTTTGTAAAAATGAATAAATAATGTCACAGACTCTCC	2700
Qy	2701	AAATTAATTAGTAAGGATTCATCCTTAATCCCTGCTAGTFTTAAGCGCTGCCTAAGTCACATTT	2760
Db	2701	AATTAATTAGTAAGGATTCATCCTTAATCCCTGCTAGTFTTAAGCGCTGCCTAAGTCACATTT	2760
Qy	2761	ACTAAAGAGATCTTTGGTTAACTCAGTATTTTAAACATCTGTGCAGCTTATGTAGGTAAGAAGT	2820
Db	2761	ACTAAAGAGATCTTTGGTTAACTCAGTATTTTAAACATCTGTGCAGCTTATGTAGGTAAGAAGT	2820
Qy	2821	AGAAGCATGTTGTACACGTGCTTGATGTTATAGTGACACAGCTTTCCTATGTTGAGATYCTCA	2880
Db	2821	AGAAGCATGTTGTACACGTGCTTGATGTTATAGTGACACAGCTTTCCTATGTTGAGATYCTCA	2880
Qy	2881	TATCATCTGTATCTTAAAGTTTCAATGTAGTFTTTACCCTTAGSANTGAATTAAGATGCTAT	2940
Db	2881	TATCATCTGTATCTTAAAGTTTCAATGTAGTFTTTACCCTTAGGATGATTAAGATGCTAT	2940
Qy	2941	ATAGGACAAAAGTTAAGTCTTTCCCTCACTACATTTGTTTCTTGGCTAGTAATAAGTA	3000
Db	2941	ATAGGACAAAAGTTAAGTCTTTCCCTCACTACATTTGTTTCTTGGCTAGTAATAAGTA	3000
Qy	3001	GTAGATACTCTGAAATAAATGTTCTCTCAAGATCCTTAAACCTCTTGGAATAATTATAA	3060
Db	3001	GTAGATACTCTGAAATAAATGTTCTCTCAAGATCCTTAAACCTCTTGGAATAATTATAA	3060
Qy	3061	AAATATTGGCAAGAAAAGAAGATAGTGTGTTTAAATATTTTTTAAAAAACACTTGAATAAG	3120
Db	3061	AAATATTGGCAAGAAAAGAAGATAGTGTGTTTAAATATTTTTTAAAAAACACTTGAATAAG	3120
Qy	3121	AATCAGTAGGGTATAAECTAGAAAGTTTAAAAATGCCCTCATAGAAGCTCCAGGGTTTACAT	3180
Db	3121	AATCAGTAGGGTATAAECTAGAAAGTTTAAAAATGCCCTCATAGAAGCTCCAGGGTTTACAT	3180
Qy	3181	TACAAGATYCTCACAAACAAACCCATGTAGAGGTGAGTAAGGCATGTTACTACAGAGGAA	3240
Db	3181	TACAAGATYCTCACAAACAAACCCATGTAGAGGTGAGTAAGGCATGTTACTACAGAGGAA	3240
Qy	3241	AGTTTGAGAGTAAACCTGTA AAAAATAATATTTTGTGTTACTTCTTAAGGAAAAGTA	3300
Db	3241	AGTTTGAGAGTAAACCTGTA AAAAATAATATTTTGTGTTACTTCTTAAGGAAAAGTA	3300
Qy	3301	TTGTTATGTTCTCCTAACCTCTGTGATTACTACTTTAAGTGATATTCATTTAAACATTT	3360
Db	3301	TTGTTATGTTCTCCTAACCTCTGTGATTACTACTTTAAGTGATATTCATTTAAACATTT	3360
Qy	3361	GCAAAATTTATTTTATTTTATTTTAAATTTCTTTTGGATGGAGTCTGCTTGTCCACCAGG	3420
Db	3361	GCAAAATTTATTTTATTTTATTTTAAATTTCTTTTGGATGGAGTCTGCTTGTCCACCAGG	3420
Qy	3421	CTGGAGTGCAGTGGAGTGATCTGCTCACTGCAACCTCCGCCCTTCGCGGTTC AAGCGAT	3480
Db	3421	CTGGAGTGCAGTGGAGTGAICTGCTCACTGCAACCTCCGCCCTTCGCGGTTC AAGCGAT	3480
Qy	3481	TCCTGCGCTCAGCTTCCCTGAGTAGCTGGAATTAACAGGCAGGTGCCACCATGCCCCACTA	3540
Db	3481	TCCTGCGCTCAGCTTCCCTGAGTAGCTGGAATTAACAGGCAGGTGCCACCATGCCCCACTA	3540
Qy	3541	ATTTTTTTTTTATTTTATTTAGTAGAGCGGGTTTCCACCATGTTGGCCAGGCTGGTATCAAAC	3600
Db	3541	ATTTTTTTTTTATTTTATTTAGTAGAGCGGGTTTCCACCATGTTGGCCAGGCTGGTATCAAAC	3600
Qy	3601	TCTGTGACCTCAGAGATCCACTCGCTTGGCCCTCCCRAAGTGTGGGATACAGGCTTGA	3660
Db	3601	TCTGTGACCTCAGAGATCCACTCGCTTGGCCCTCCCRAAGTGTGGGATACAGGCTTGA	3660
Qy	3661	GCCACCAACGCCGGCTAAAAACATTCGAAATTTAAATGAGAGTGTAAAAATTAATAATG	3720
Db	3661	GCCACCAACGCCGGCTAAAAACATTCGAAATTTAAATGAGAGTGTAAAAATTTAAATAATG	3720
Qy	3721	ACTGCGCCTGTTCTGTTTTAGTATGTAATCCTCAGTGTCTTCACCTTTGACATGTCGTGCC	3780

Db	3721	ACTGCCCTGTTCTGTTTGTAGTAAATGCTCAGTTCTTACCTTTGCAGCTGTCGTGCC	3780
Qy	3781	ACTTAGTTTGGTTATATAGTCAATTAACCTGAAATTTGGTCTGTATAGTCTAGACTTTAAAT	3840
Db	3781	ACTTAGTTTGGTTATATAGTCAATTAACCTGAAATTTGGTCTGTATAGTCTAGACTTTAAAT	3840
Qy	3841	TTAAAGTTTCTACAAAGGGGAGAAAAGTGTTAAAAATTTTAAAAATATGTTTTCCAGGACA	3900
Db	3841	TTAAAGTTTCTACAAAGGGGAGAAAAGTGTTAAAAATTTTAAAAATATGTTTTCCAGGACA	3900
Qy	3901	CTTCACCTCCAAGTCAGGTAGGTAGTTCAATCTAGTTGTGTAGCCAAGGACTCAAGGACTG	3960
Db	3901	CTTCACCTCCAAGTCAGGTAGGTAGTTCAATCTAGTTGTGTAGCCAAGGACTCAAGGACTG	3960
Qy	3961	AAATGTTTTAAACATAAGGCTTTTCCCTGTTCTGGAGCGGCACATTCATTAATAATCTCTCTA	4020
Db	3961	AAATGTTTTAAACATAAGGCTTTTCCCTGTTCTGGAGCGGCACATTCATTAATAATCTCTCTA	4020
Qy	4021	AAACTTGATGTTTAGAGTTAAGCAAGACTTTTTTTTCTCTCCTCCATGAGTTGTGAAAT	4080
Db	4021	AAACTTGATGTTTAGAGTTAAGCAAGACTTTTTTTTCTCTCCTCCATGAGTTGTGAAAT	4080
Qy	4081	TTAATGCCAACAGCTCATGTGGCTACAAAGTTTATTTTAAAGATTTGTTTAAATAATGCTGT	4140
Db	4081	TTAATGCCAACAGCTCATGTGGCTACAAAGTTTATTTTAAAGATTTGTTTAAATAATGCTGT	4140
Qy	4141	TGCTTCAGGTCTTAAAAATCAGTCAGCACTCCAACTTCTAATCAAAATTTTGGAGACTTA	4200
Db	4141	TGCTTCAGGTCTTAAAAATCAGTCAGCACTCCAACTTCTAATCAAAATTTTGGAGACTTA	4200
Qy	4201	ACAGCATATTTGCTGTTTGAACATATAAAAGCACCAGGATCTTTTCCATCTAATTCGCA	4260
Db	4201	ACAGCATATTTGCTGTTTGAACATATAAAAGCACCAGGATCTTTTCCATCTAATTCGCA	4260
Qy	4261	AAAATTGATCATTTGCAAAAGTCAAAACCTAGCCATATCCAAATCTTTTCCCTCCCAA	4320
Db	4261	AAAATTGATCATTTGCAAAAGTCAAAACCTAGCCATATCCAAATCTTTTCCCTCCCAA	4320
Qy	4321	GAGTTCTCAGTGCTACATGTAGACTATTCTCTTTCTGTATAAGTTTCACCTCAGGATTT	4380
Db	4321	GAGTTCTCAGTGCTACATGTAGACTATTCTCTTTCTGTATAAGTTTCACCTCAGGATTT	4380
Qy	4381	CAAGTCACCACCTATTTTACATTTTAGTCATGCAAAAGATTCAAGTAGTTTGCATAATAGT	4440
Db	4381	CAAGTCACCACCTATTTTACATTTTAGTCATGCAAAAGATTCAAGTAGTTTGCATAATAGT	4440
Qy	4441	ACTATCTTTATTTGTAATAATTTAGTCGCTGCATCAAAAGCATTTGCTTAATTTTGAG	4500
Db	4441	ACTATCTTTATTTGTAATAATTTAGTCGCTGCATCAAAAGCATTTGCTTAATTTTGAG	4500
Qy	4501	AACTGGTTTTAGCATTTACAACTAAATTCAGTTTAATTAATTAAGTCTTTATATTGCC	4560
Db	4501	AACTGGTTTTAGCATTTACAACTAAATTCAGTTTAATTAATTAAGTCTTTATATTGCC	4560
Qy	4561	TTTCTGCTACATTTGGTTTTTTTCCCTGCTCCCTTTGATTACGGGCTAAGGTAGGTAAG	4620
Db	4561	TTTCTGCTACATTTGGTTTTTTTCCCTGCTCCCTTTGATTACGGGCTAAGGTAGGTAAG	4620
Qy	4621	ANNGGTGTAGTGAGTGATATAATGTGATTTGGCCCTGTGTATATATGATATTTTGTAT	4680
Db	4621	ANNGGTGTAGTGAGTGATATAATGTGATTTGGCCCTGTGTATATATGATATTTTGTAT	4680
Qy	4681	TTTTGTGTTATATATTTACATTTCCAGTAGTTGTTTTTGTGCTGTTCCATTTTAGGGAT	4740
Db	4681	TTTTGTGTTATATATTTACATTTCCAGTAGTTGTTTTTGTGCTGTTCCATTTTAGGGAT	4740
Qy	4741	AAAAATTTGATTTTGAACATGAATGGAGACTACCGCCCGCAGCATTTAGTTTCACATGATA	4800
Db	4741	AAAAATTTGATTTTGAACATGAATGGAGACTACCGCCCGCAGCATTTAGTTTCACATGATA	4800
Qy	4801	TACCTTTTAAACCCGAATCATTTGTTTTTATTTCTGATTTACACAGGTGTTGAATGGGAAA	4860
Db	4801	TACCTTTTAAACCCGAATCATTTGTTTTTATTTCTGATTTACACAGGTGTTGAATGGGAAA	4860



Db 1141 ATCTCCAAAATCCTATGGTACAAGAGCTATACGAATAGGGGTCAGTTTCAAGGACATT 1200  
Qy 1201 AAGAAAATAATGGAGAAAAAATTCAGATATCTGGAGCAACTATAAATCACTTCAGGTT 1260  
Db 1201 AAGAAAATAATGGAGAAAAAATTCAGATATCTGGAGCAACTATAAATCACTTCAGGTT 1260  
Qy 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGT 1320  
Db 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGT 1320  
Qy 1321 TCATTACAGAAGAGATTAGTACTGAGAGCAGCTAGGCGCCGCAAGAGAGAGAGCTT 1380  
Db 1321 TCATTACAGAAGAGATTAGTACTGAGAGCAGCTAGGCGCCGCAAGAGAGAGAGCTT 1380  
Qy 1381 TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTGTCTGTGTCGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTGTCTGTGTCGACATCTAGTC 1440  
Qy 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCAATTACT 1500  
Db 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCAATTACT 1500  
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Db 1501 TTCAAGCAAAAAATTTTATCTCTTAATCTAATCTATAGTAGGCATGTTATGTTCT 1560  
Qy 1561 TATTACCTGATGAATGTGTGATGTGAACGTACTTTAAGTAATCAGGATTGAATTCAT 1620  
Db 1561 TATTACCTGATGAATGTGTGATGTGAACGTACTTTAAGTAATCAGGATTGAATTCAT 1620  
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Db 1621 TAGCATTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTAGTTGGCAATATA 1680  
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Db 1681 ATCTTTGAATTTCTGATTTTCAGGTAATAGCTGTATTAATCCATTTTTTACTGTTA 1740  
Qy 1741 TTTAATTTGAAACCATPAGACTAAGATAAGAAGCATCATPACTATACTGAACACAAATGCT 1800  
Db 1741 TTTAATTTGAAACCATPAGACTAAGATAAGAAGCATCATPACTATACTGAACACAAATGCT 1800  
Qy 1801 ATTCAATGATACGATTTAATTTCTAAGTGTAACTGAATTAATCACTGGAATTTTAT 1860  
Db 1801 ATTCAATGATACGATTTAATTTCTAAGTGTAACTGAATTAATCACTGGAATTTTAT 1860  
Qy 1861 TCCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
Db 1861 TCCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
Qy 1921 ATCTCCCAATCACATAATTTGTTGTGTGAAAGGAATAAATGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCAATCACATAATTTGTTGTGTGAAAGGAATAAATGTTCCATGCTGGTG 1980  
Qy 1981 GAAAGATAGAGATTGTTTTAGAGTTGGTTGTGTTTTAGGATCTGTCGCAATTTTCT 2040  
Db 1981 GAAAGATAGAGATTGTTTTAGAGTTGGTTGTGTTTTAGGATCTGTCGCAATTTTCT 2040  
Qy 2041 TTTAAAGTATTAACACGCTACTTGTGCAATTAATTTTTAAAGTATGTCCTATTTTG 2100  
Db 2041 TTTAAAGTATTAACACGCTACTTGTGCAATTAATTTTTAAAGTATGTCCTATTTTG 2100  
Qy 2101 AAAGCGTATTTAATGATAGATACTATCGAGCCCAACATGTACTGACATGGAAGATGTCA 2160  
Db 2101 AAAGCGTATTTAATGATAGATACTATCGAGCCCAACATGTACTGACATGGAAGATGTCA 2160  
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Db 2161 AAGATATGTTAAGTGTAAATTCAGTGGCAAAACACATPATATAGTCTGAGCCAGATCA 2220  
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Db 2221 AAGTATGATCTTTTAAATATGATAGCAAAAGATTTGGAAGATATACACCAACTG 2280

Qy 2281 TTAATGTGGTTTTCTTTCGGGAGGGGGGATTGGGGAGGGCCCCCAGAGGGTTTTTA 2340  
Db 2281 TTAATGTGGTTTTCTTTCGGGAGGGGGGATTGGGGAGGGCCCCCAGAGGGTTTTTA 2340  
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Qy 2401 GTATTACTTTTGTAAATCAGAAATTTTGAAGAGTATTTTGTCTGATTAAAGCTTAGGCAT 2460  
Db 2401 GTATTACTTTTGTAAATCAGAAATTTTGAAGAGTATTTTGTCTGATTAAAGCTTAGGCAT 2460  
Qy 2461 GTTCAAAAGCGCTGCACAAACTACTTATCACTCAGCTTTAGTTTTCTAATCCAAGAGCA 2520  
Db 2461 GTTCAAAAGCGCTGCACAAACTACTTATCACTCAGCTTTAGTTTTCTAATCCAAGAGCA 2520  
Qy 2521 GGGCAGTTAACTTTTGGTGCCCAATGTGAATGTAAATGATTATGTTTTTCTGCTT 2580  
Db 2521 GGGCAGTTAACTTTTGGTGCCCAATGTGAATGTAAATGATTATGTTTTTCTGCTT 2580  
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Db 2581 TGTGATGAAAAATATTTCTCAGTGGTAGTTTGTGACAGGTAGACCATGCTTATCTTG 2640  
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Db 2701 AATTAAATTAGTAAGGATTCATCTTAATCTTGTAGTTTAAAGCTGCTTAAGTCACATT 2760  
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Db 2761 ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAGT 2820  
Qy 2821 AGAAGCATGTTTGTACACTGCTGTGTAGTTATAGTGACAGCTTTCATGTTGAGATCTCA 2880  
Db 2821 AGAAGCATGTTTGTACACTGCTGTGTAGTTATAGTGACAGCTTTCATGTTGAGATCTCA 2880  
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Db 2881 TATCATCTTGTATCTTAAAGTTTCAATGAGTTTACCCTTAGGATGATTAAAGTAT 2940  
Qy 2941 ATAGCAAAAATGTTAAGTCTTCTCTACCTACATTTGTTTCTTGGCTAGTAAATAGTA 3000  
Db 2941 ATAGCAAAAATGTTAAGTCTTCTCTACCTACATTTGTTTCTTGGCTAGTAAATAGTA 3000  
Qy 3001 GTAGATCTTCTGAAATAAATGTTCTCAAGATGCTTAAACCTCTTTGGAATTTATAA 3060  
Db 3001 GTAGATCTTCTGAAATAAATGTTCTCAAGATGCTTAAACCTCTTTGGAATTTATAA 3060  
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Db 3061 AATATTGCAAGAAAAAGAAAGTATGTTTAAATATTTTTTAAAAACACTTGAATAG 3120  
Qy 3121 AATCAGTAGGATTAACACTAGAAATGCTTAAATGCTCATAGAGCTCCAGGTTTACAT 3180  
Db 3121 AATCAGTAGGATTAACACTAGAAATGCTTAAATGCTCATAGAGCTCCAGGTTTACAT 3180  
Qy 3181 TACAAGATTCTCACAAACCAACCCATTTAGAGGTGAGTAAGGCATGTTTACTACAGAGAA 3240  
Db 3181 TACAAGATTCTCACAAACCAACCCATTTAGAGGTGAGTAAGGCATGTTTACTACAGAGAA 3240  
Qy 3241 AGTTTGAGAGTAAACTGTATAAATAATATTTTGTGTTACTTCTTAAGAGAAAGATA 3300  
Db 3241 AGTTTGAGAGTAAACTGTATAAATAATATTTTGTGTTACTTCTTAAGAGAAAGATA 3300  
Qy 3301 TTGTTATCTTCTTAACTTCTGTTGATTACTTAAAGTATGATTTTCAATTTAAACATT 3360  
Db 3301 TTGTTATCTTCTTAACTTCTGTTGATTACTTAAAGTATGATTTTCAATTTAAACATT 3360

Db	4441	ACCTTATCTTTATTTGTAATAAATTTAGTCGCGATCAAAAGCATTTGCTTAATTTTTCGAG	4500
Qy	4501	AACTGGTTTTAGCATTTACAAACTAAATCCAGTTAAATTAATTAATAGCTTTATATGCC	4560
Db	4501	AACTGGTTTTAGCATTTACAAACTAAATCCAGTTAAATTAATTAATAGCTTTATATGCC	4560
Qy	4561	TTTCCTGCTACATTTGGTTTTTTTCCCTGTCCTCTTTGATTTACGGGCTAAGSTAGGTAAAG	4620
Db	4561	TTTCCTGCTACATTTGGTTTTTTTCCCTGTCCTCTTTGATTTACGGGCTAAGSTAGGTAAAG	4620
Qy	4621	ANNGGGTGTAAGTCAGTCGTATATAATGTAATTTGGCCCTGCTGTATATGATATTTTGTATT	4680
Db	4621	ANNGGGTGTAAGTCAGTCGTATATAATGTAATTTGGCCCTGCTGTATATGATATTTTGTATT	4680
Qy	4681	TTTTTGTGTTATATATTTACATTTTCAGTAGTTGTTTTTTTGTGTTTCCATTTTACGGGAT	4740
Db	4681	TTTTTGTGTTATATATTTACATTTTCAGTAGTTGTTTTTTTGTGTTTCCATTTTACGGGAT	4740
Qy	4741	AAAAATTTGTAATTTGAACTATGAATGGAGACTACCGCCCCAGCATTTAGTTTCACATGATA	4800
Db	4741	AAAAATTTGTAATTTGAACTATGAATGGAGACTACCGCCCCAGCATTTAGTTTCACATGATA	4800
Qy	4801	TACCTTTTAAACCCGAATCATTTGTTTTATTTCTGTATTCACAGGTGTTGTAATGGGGAAA	4860
Db	4801	TACCTTTTAAACCCGAATCATTTGTTTTATTTCTGTATTCACAGGTGTTGTAATGGGGAAA	4860
Qy	4861	GGGGCTAGTATATCAGTAGGATATACATATGGGATGTATATATATCATTTGCTGTTAGACAA	4920
Db	4861	GGGGCTAGTATATCAGTAGGATATACATATGGGATGTATATATATCATTTGCTGTTAGACAA	4920
Qy	4921	ATGAAATTTAAATGGGGCTGGGCTCAGTGGCTCAGCGCTCTAATCCAGCACATTTGGGAGG	4980
Db	4921	ATGAAATTTAAATGGGGCTGGGCTCAGTGGCTCAGCGCTCTAATCCAGCACATTTGGGAGG	4980
Qy	4981	CTGAGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCATCTCTGGCTAACACGGSTGAAC	5040
Db	4981	CTGAGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCATCTCTGGCTAACACGGSTGAAC	5040
Qy	5041	CCGCTCTCTACTAAAAACAGAAAAATTTAGCCGGCGGTGGTGGCGGGCGCTGTAGTCCCA	5100
Db	5041	CCGCTCTCTACTAAAAACAGAAAAATTTAGCCGGCGGTGGTGGCGGGCGCTGTAGTCCCA	5100
Qy	5101	GCTACTCGGAGGCTCAGGCGAGGAGAAATGGTGTGAACCCGGGAGCGAGAGCTTCGAGTGA	5160
Db	5101	GCTACTCGGAGGCTCAGGCGAGGAGAAATGGTGTGAACCCGGGAGCGAGAGCTTCGAGTGA	5160
Qy	5161	GCCGAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAA	5220
Db	5161	GCCGAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAA	5220
Qy	5221	AAAAAAAAAAG 5232	
Db	5221	AAAAAAAAAAG 5232	

RESULT 4  
US-08-511-485-3  
: Sequence 3, Application US/08511485  
: Patent No. 5919912  
: GENERAL INFORMATION:  
: APPLICANT: Korneluk, Robert G.  
: APPLICANT: Mackenzie, Alexander E.  
: APPLICANT: Baird, Stephen  
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
: TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
: NUMBER OF SEQUENCES: 38  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Fish & Richardson P.C.  
: STREET: 225 Franklin Street  
: CITY: Boston  
: STATE: MA  
: COUNTRY: USA

ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511.485  
FILING DATE: 04-AUG-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07540/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2540 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: DNA (genomic)  
US-08-511-485-3

Query Match 38.0%; Score 1990; DB 2; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 GAAAGGTGGACAGTCTCTATTTTCAAGAGAGATGACTTTTAAACAGTCTTTGAAGGATCT 60  
Qy 61 AAAACTTGTGTACCTGCGACATCAATTAAGGAAGAAGATTTGTAGAAGAGTTTAATAGA 120  
Db 61 AAAACTTGTGTACCTGCGACATCAATTAAGGAAGAAGATTTGTAGAAGAGTTTAATAGA 120  
Qy 121 TAAAAACTTTTGTCTTAACTTTTCAAGTGGTGTCTCTGTTTTCAGCATCAACACTGGCAGCA 180  
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Qy 181 GCAGGGTTCTTTTATACGTGGTGAAGAGATACCGTGCAGTCTTTAGTTGTCATGACGCT 240  
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Qy 241 GTAGATAGATGGCAATATGGAGACTTCAGCAGTGGGAAGACACAGGAAAGTATCCCAAT 300  
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Qy 301 TGCAGATTTATCAACGGCTTTTATCTTCAAAATAGTGCACGAGTCTACAAATTTCTGGT 360  
Db 301 TGCAGATTTATCAACGGCTTTTATCTTCAAAATAGTGCACGAGTCTACAAATTTCTGGT 360  
Qy 361 ATCCAGAAATGGTCACTACAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGCCTTA 420  
Db 361 ATCCAGAAATGGTCACTACAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGCCTTA 420  
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Db 421 GACAGGCCATCTGAGACACATGCGACATCTTTTGAAGTGGCAGGTTGTAGATATA 480  
Qy 481 TCAGACACATATACCCGAGGAACCTGCCATGTATGTAGTGAAGAGCTAGATTAAGTCC 540  
Db 481 TCAGACACATATACCCGAGGAACCTGCCATGTATGTAGTGAAGAGCTAGATTAAGTCC 540  
Qy 541 TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
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Qy 601 TACTACACAGTATTTGGTACCAAGTGCAGTCTTTTGGTGGTGGGAAACTGAAAAAT 660  
Db 601 TACTACACAGTATTTGGTACCAAGTGCAGTCTTTTGGTGGTGGGAAACTGAAAAAT 660

Db 601 TACTACACAGTATTTGGTACCAAGTGCAGTCTTTTGGTGGTGGGAAACTGAAAAAT 660  
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Db 661 TGGGAACCTTGTGATCGTCCCTGGTGCAGAACACAGCGACACTTTCCCTAAATGCTTCTTT 720  
Qy 721 GTTTTGGCCCGAATCTTAATATTTCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAT 780  
Db 721 GTTTTGGCCCGAATCTTAATATTTCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAT 780  
Qy 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATATGAAGCAGGATC 840  
Db 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATATGAAGCAGGATC 840  
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Db 901 TATGCTTTAGGTGAAGGTGATAAAGTCTCTTCTACTTGTGGAGGAGGGCTAACTGAT 960  
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Db 1021 CTGTTAGAACAGAGGAGCAAGATATATAACAATATTTCAATTAACCTCACTTCTGAG 1080  
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Db 1081 GAGTCTCTGGTGAAGAACTACTTACCAAGAACACCATCACTAAGTGAAGAAATTTGATGATACC 1140  
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Db 1201 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTCAAGGTT 1260  
Qy 1261 CTGTTGTCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
Db 1261 CTGTTGTCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
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Db 1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGCGCCTGCAAGAGGAGAGCTT 1380  
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Db 1381 TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTTTGTTCCTTGTGGACATCTAGTC 1440  
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Db 1441 ACTTGTAAACAAATGCTGAAGCAGTTGACAAAGTCCCATGTGCTACACAGTCAATTA 1500  
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Db 1501 TTCAGCAAAATTTTATGCTTAACTACTATAGTAGGAGCATGTTATGTTGTTCT 1560  
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Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTTGATTTTTCAGGTTATAGCTGATTAATCCATTTTTTTTACTGTTA 1740  
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QY 1741 TTTAAATTGAACCATAGACTAAGAATAAAGAAGCATCATACTATAACTGAACAAATGTGT 1800  
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Db 1741 TTTAAATTGAACCATAGACTAAGAATAAAGAAGCATCATACTATAACTGAACAAATGTGT 1800  
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Db 1801 ATTCATAGTATAGTGAATTAATTTCTTAAGTGAAGTGAATTAATCAATCTGGATTTTTTAT 1860  
QY 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
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Db 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
QY 1921 ATCTCCCAATCACATAATTTGTTTGTGTGAAAAAGGAATAAATTTGCCATGCTGGTG 1980  
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Db 1921 ATCTCCCAATCACATAATTTGTTTGTGTGAAAAAGGAATAAATTTGCCATGCTGGTG 1980  
QY 1981 GAAAGATAGAGATTGTTTATAGAGTTGGTTGTGTGTTTATAGGATCTGTCATTTTCT 2040  
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Db 1981 GAAAGATAGAGATTGTTTATAGAGTTGGTTGTGTGTTTATAGGATCTGTCATTTTCT 2040  
QY 2041 T 2041  
|  
Db 2041 T 2041

RESULT 5  
US-09-392-580-1  
; Sequence 1, Application US/09392580  
; Patent No. 6087173  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Elizabeth J. Ackermann  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION  
; FILE REFERENCE: RTS-0072  
; CURRENT APPLICATION NUMBER: US/09/392,580  
; CURRENT FILING DATE: 1999-09-09  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 1  
; LENGTH: 2540  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (34)..(1527)  
US-09-392-580-1

Query Match 38.0%; Score 1990; DB 3; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGTGGACAAGTCCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT 60  
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Db 1 GAAAGGTGGACAAGTCCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT 60  
QY 61 AAAAATTTGTACTCGACATCAATAGGAAGAAGAATTTCTAGAAGAGTTTAATAGA 120  
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Db 61 AAAAATTTGTACTCGACATCAATAGGAAGAAGAATTTCTAGAAGAGTTTAATAGA 120  
QY 121 TTAATAAATTTTGTCTAATTTTCCAAAGTGTAGTCCCTGTTTTCAGCATCAACACTGGCACGA 180  
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Db 121 TTAATAAATTTTGTCTAATTTTCCAAAGTGTAGTCCCTGTTTTCAGCATCAACACTGGCACGA 180  
QY 181 GCAGGTTTCTTTATCTGTGTGAAGGAGATACCGTGGGTGCTTTTATGTTGTCATGAGCT 240  
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Db 181 GCAGGTTTCTTTATCTGTGTGAAGGAGATACCGTGGGTGCTTTTATGTTGTCATGAGCT 240  
QY 241 GTAGATAGTGGCAATATGGAGACTCAGCAGTTGGGAAGACACAGGAAGATATCCCAAT 300  
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Db 241 GTAGATAGTGGCAATATGGAGACTCAGCAGTTGGGAAGACACAGGAAGATATCCCAAT 300  
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAAATAGTGCCACGAGCTACAAATTTCTGTT 360

Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAAATAGTGCCACGAGTCTACAAATTTCTGTT 360  
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QY 361 ATCCAGAAATGGTCAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCAATTTGCTTTA 420  
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Db 361 ATCCAGAAATGGTCAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCAATTTGCTTTA 420  
QY 421 GACAGGCCATCTCGAGACACATGCAGACTATCTTTTTCAGAACTGGGAGGTTGTAGATATA 480  
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Db 421 GACAGGCCATCTCGAGACACATGCAGACTATCTTTTTCAGAACTGGGAGGTTGTAGATATA 480  
QY 481 TCAGACACCATATACCCGAGGAACCCCTGCCATGTATAGTGAAGAAGTAGATTAAAGTCC 540  
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Db 481 TCAGACACCATATACCCGAGGAACCCCTGCCATGTATTTGTGAAGAAGTAGATTAAAGTCC 540  
QY 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCAGAGAGTTAGCAAGTGGTGGACT 600  
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Db 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCAGAGAGTTAGCAAGTGGTGGACT 600  
QY 601 TACTACACAGTATTTGGTGACCAAGTGCAGTGTCTTTTGTGTGTGGTGGTGGTGGTGGT 660  
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Db 601 TACTACACAGTATTTGGTGACCAAGTGCAGTGTCTTTTGTGTGTGGTGGTGGTGGTGGT 660  
QY 661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGGGACACTTTCCTAATTTGCTTTT 720  
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Db 661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGGGACACTTTCCTAATTTGCTTTT 720  
QY 721 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGCTGATGATGATGAT 780  
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Db 721 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGCTGATGATGATGAT 780  
QY 781 TTCCCAAAATTCACAAATCTTCCCAAGAAATCCATCCATGGCAGATTTATGAAGCACGGATC 840  
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Db 781 TTCCCAAAATTCACAAATCTTCCCAAGAAATCCATCCATGGCAGATTTATGAAGCACGGATC 840  
QY 841 TTTTACTTTTGGGACATGGATATCTCAGTTTAAACAAGGAGCAGCTTGCAGAGCTGGATTT 900  
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Db 841 TTTTACTTTTGGGACATGGATATCTCAGTTTAAACAAGGAGCAGCTTGCAGAGCTGGATTT 900  
QY 901 TATGCTTTTAGTGAAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 960  
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Db 901 TATGCTTTTAGTGAAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 960  
QY 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACTGCTAAATGGTATCCAGGCTGCAATAT 1020  
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Db 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACTGCTAAATGGTATCCAGGCTGCAATAT 1020  
QY 1021 CTGTTAGACAGAAAGGACAAAGATATATAAACAATATTCATTTAATCTCATTTGAG 1080  
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Db 1021 CTGTTAGACAGAAAGGACAAAGATATATAAACAATATTCATTTAATCTCATTTGAG 1080  
QY 1081 GAGTGTCTGTAAGAATCTGAGAAACACCCTACTAATAGAGAAATTTGATGATGATGAT 1140  
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Db 1081 GAGTGTCTGTAAGAATCTGAGAAACACCCTACTAATAGAGAAATTTGATGATGATGAT 1140  
QY 1141 ATCTTCCAAAATCCTATGGTACAAAGAGCTATACGAATGGGTTTCAGTTTCAAGGACAT 1200  
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Db 1141 ATCTTCCAAAATCCTATGGTACAAAGAGCTATACGAATGGGTTTCAGTTTCAAGGACAT 1200  
QY 1201 AAGAAATATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCCTTTGAGGTT 1260  
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Db 1201 AAGAAATATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCCTTTGAGGTT 1260  
QY 1261 CTGGTTCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAAGT 1320  
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Db 1261 CTGGTTCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAAGT 1320  
QY 1321 TCATTACAGAAAGAGATTAGTACTGAGAGCAGCTAGAGCCCTGCAAGAGGAGAACT 1380  
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Db 1321 TCATTACAGAAAGAGATTAGTACTGAGAGCAGCTAGAGCCCTGCAAGAGGAGAACT 1380  
QY 1381 TGCAAAATCTGTATGGATAGAAATATTTGCTTATGCTTTTGTCTTGTGACATCTAGT 1440  
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Db 1381 TGC AAAATCTGTATGATAGAAAATATTGCTATCGTTTGTTCCTTGTGGACATCTAGTC 1440
Qy 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAAGTGTCCTCATGTCTACACAGTCATTACT 1500
Db 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAAGTGTCCTCATGTCTACACAGTCATTACT 1500
Qy 1501 TTCAAGCAAAAATTTTATGCTCTTAATCTAACTAATCTATAGTAGGCATGTTATGTTGTTCT 1560
Db 1501 TTCAAGCAAAAATTTTATGCTCTTAATCTAACTAATCTATAGTAGGCATGTTATGTTGTTCT 1560
Qy 1561 TATTACCCGTGAATGAATGTGTGATGTGAACGTGACTTTAAAGTAATCAGAGTTGAATTCAT 1620
Db 1561 TATTACCCGTGAATGAATGTGTGATGTGAACGTGACTTTAAAGTAATCAGAGTTGAATTCAT 1620
Qy 1621 TAGCATTTGCTACCAAGTAGAAAATAATGTCATGCGAGTGTTTAGTTGGCAATATA 1680
Db 1621 TAGCATTTGCTACCAAGTAGAAAATAATGTCATGCGAGTGTTTAGTTGGCAATATA 1680
Qy 1681 ATCTTTGAAATTTCTTGAATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTA 1740
Db 1681 ATCTTTGAAATTTCTTGAATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTA 1740
Qy 1741 TTTAATTGAACCAATAGACTAAGAAATAGAAGCATCATACTATAACTGAACACAAATGTGT 1800
Db 1741 TTTAATTGAACCAATAGACTAAGAAATAGAAGCATCATACTATAACTGAACACAAATGTGT 1800
Qy 1801 ATTCATAGTACTGATTTAATTTCTAAGTGAAGTGAATTAATCAATCTGGATTTTTTAT 1860
Db 1801 ATTCATAGTACTGATTTAATTTCTAAGTGAAGTGAATTAATCAATCTGGATTTTTTAT 1860
Qy 1861 TCTTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATATAAATGTGGAGATTAGAGTTA 1920
Db 1861 TCTTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATATAAATGTGGAGATTAGAGTTA 1920
Qy 1921 ATCTCCCCAATCACAATAATTTGTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980
Db 1921 ATCTCCCCAATCACAATAATTTGTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980
Qy 1981 GAAAGATAGAGATGTTTTTAGAGGTTGGTTGTTGTTTGGATTTCTGTCCATTTTCT 2040
Db 1981 GAAAGATAGAGATGTTTTTAGAGGTTGGTTGTTGTTTGGATTTCTGTCCATTTTCT 2040
Qy 2041 T 2041
Db 2041 T 2041

RESULT 6
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
us-09-239-867-3

Query Match 30.4%; Score 1588; DB 4; Length 1588;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT 60
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Db 1 GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTGAAGGATCT 60
Qy 61 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGATTTGTAGAGAGTTTAATAGA 120
Db 61 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGATTTGTAGAGAGTTTAATAGA 120
Qy 121 TTA AAAACTTTTGTCTAATTTTCCAAAGTGGTAGTCCTGTTTTCAGCATCAACACTGGCAGCA 180
Db 121 TTA AAAACTTTTGTCTAATTTTCCAAAGTGGTAGTCCTGTTTTCAGCATCAACACTGGCAGCA 180
Qy 181 GCAGGGTTCCTTTATCTACTGTTGAAGGAGATACCGTGC GGTCCTTTTAGTTGTCATGCGAGCT 240
Db 181 GCAGGGTTCCTTTATCTACTGTTGAAGGAGATACCGTGC GGTCCTTTTAGTTGTCATGCGAGCT 240
Qy 241 GTAGATAGATGGCAATATGAGAGACTCAGCAGTTGGAGACACAGAGAAAGTATCCCCAAAT 300
Db 241 GTAGATAGATGGCAATATGAGAGACTCAGCAGTTGGAGACACAGAGAAAGTATCCCCAAAT 300
Qy 301 TGCAGATTTATCAACGGCTTTTATCTTGA AAATAGTGCACGCACTCTACAAATTTCTGGT 360
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGA AAATAGTGCACGCACTCTACAAATTTCTGGT 360
Qy 361 ATCCAGAATGTCAGTACAAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGGCCCTTA 420
Db 361 ATCCAGAATGTCAGTACAAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGGCCCTTA 420
Qy 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGCGAGTTGTAGATATA 480
Db 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGCGAGTTGTAGATATA 480
Qy 481 TCAGACACCATATATACCGGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540
Db 481 TCAGACACCATATATACCGGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTTAAAGTCC 540
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Db 541 TTTCAGAACTGGCCAGACTATGCTACACTAACCCCAAGAGAGTTAGCAAGTGTCTGGAGCTC 600
Qy 601 TACTACACAGATTTGTTGACCAAGTGCAGTGCTTTTGTGTTGGTGGAAAACTGAAAAAT 660
Db 601 TACTACACAGATTTGTTGACCAAGTGCAGTGCTTTTGTGTTGGTGGAAAACTGAAAAAT 660
Qy 661 TGGGAACCTTGTGATCGTGCCTGCTCAGACACACAGGCGACACTTTTCTCTTAATTGCTCTTT 720
Db 661 TGGGAACCTTGTGATCGTGCCTGCTCAGACACACAGGCGACACTTTTCTCTTAATTGCTCTTT 720
Qy 721 GTTTTGGCCCGGAATCTTAATATTTCGAAGTGAATCTGATGCTGTGATGTTCTGATAGGAAT 780
Db 721 GTTTTGGCCCGGAATCTTAATATTTCGAAGTGAATCTGATGCTGTGATGTTCTGATAGGAAT 780
Qy 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTTAAGAGCAGGATC 840
Db 781 TTCCCAAAATTCACAAATCTTCCAAAGAAATCCATCCATGGCAGATTTAAGAGCAGGATC 840
Qy 841 TTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTTGCAGAGCTGGATTT 900
Db 841 TTTACTTTTGGGACATGGATATACTCAGTTAAACAGGAGCAGCTTGCAGAGCTGGATTT 900
Qy 901 TATGCTTTTAGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGAGGAGGCTTAACGTAT 960
Db 901 TATGCTTTTAGTGAAGTGATAAAGTAAAGTGCCTTTCACTGTGGAGGAGGCTTAACGTAT 960
Qy 961 TGGAGGCCAGTGAAGACCTTTGGGAACAACATGCTAAATGTTATCCAGGTTGCAAAATAT 1020
Db 961 TGGAGGCCAGTGAAGACCTTTGGGAACAACATGCTAAATGTTATCCAGGTTGCAAAATAT 1020
Qy 1021 CTGTTAGAACAGAAGGGACAAGAATATATAAACAAATATTTCACTTAACCTCACTCTGAG 1080
Db 1021 CTGTTAGAACAGAAGGGACAAGAATATATAAACAAATATTTCACTTAACCTCACTCTGAG 1080
Qy 1081 GAGTGTCTGGTAAAGAACTACTGAGAAAAACACCACTCACTAAGTAGAAGATTTGATGATACC 1140
Db 1081 GAGTGTCTGGTAAAGAACTACTGAGAAAAACACCACTCACTAAGTAGAAGATTTGATGATACC 1140
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Db 1081 GAGTGTCTGGTAAGAACTACTGTAGAAACACCACATCACTAACTAGAGAAATGTGATGATACC 1140
QY 1141 ATCTTCAAAATCCTATGGTACAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATT 1200
Db 1141 ATCTTCAAAATCCTATGGTACAGAGCTATACGAATGGGTTTCAGTTTCAAGGACATT 1200
QY 1201 AAGAAATATGAGGAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT 1260
Db 1201 AAGAAATATGAGGAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT 1260
QY 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAGACAGATATGCAAGATGAGTCAAGTCAAGT 1320
Db 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAGACAGATATGCAAGATGAGTCAAGTCAAGT 1320
QY 1321 TCATTACAGAAAGAGATTAGTACTGAAGACAGCTAAGGCGCTGCAAGAGGAGAGAGCTT 1380
Db 1321 TCATTACAGAAAGAGATTAGTACTGAAGACAGCTAAGGCGCTGCAAGAGGAGAGAGCTT 1380
QY 1381 TGCAAAATCTGTATGATAGAAATATGCTATCTGCTTCTTCTTCTGCTGACATCTAGTC 1440
Db 1381 TGCAAAATCTGTATGATAGAAATATGCTATCTGCTTCTTCTTCTGCTGACATCTAGTC 1440
QY 1441 ACTTGTAAACAATGCTGTAAGCAGTGTGACAACTGCTGCTACACAGTCAATTAAT 1500
Db 1441 ACTTGTAAACAATGCTGTAAGCAGTGTGACAACTGCTGCTACACAGTCAATTAAT 1500
QY 1501 TTCAAGCAAAATTTTATGCTTAACTTAATCTAAGTGTGCTAGGATGTTATGTTGTTCT 1560
Db 1501 TTCAAGCAAAATTTTATGCTTAACTTAATCTAAGTGTGCTAGGATGTTATGTTGTTCT 1560
QY 1561 TATTACCCCTGATTGAATGTGTGATGTA 1588
Db 1561 TATTACCCCTGATTGAATGTGTGATGTA 1588

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RESULT 7

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US-08-742-185-102/c
; Sequence 102, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,734
; FILING DATE: 31-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429
; FILING DATE: 22-SEP-1994
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH194-07A2

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40328 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-742-185-102
;
; Query Match 2.0%; Score 103; DB 3; Length 40328;
; Best Local Similarity 100.0%; Pred. No. 3.3e-31;
; Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 4955 GCCTGTAAATCCAGCACCTTTGGGAGGCTGAGGAGGTGGATCAGGAGGTTCAGGAGATCGA 5014
; Db 32275 GCCTGTAAATCCAGCACCTTTGGGAGGCTGAGGAGGTGGATCAGGAGGTTCAGGAGATCGA 32216
;
; QY 5015 GACCATCTCGCTAAACACGGTGAACCCCGTCTCTACTAAAAA 5057
; Db 32215 GACCATCTCGCTAAACACGGTGAACCCCGTCTCTACTAAAAA 32173
;
; RESULT 8
; US-08-742-185-101/c
; Sequence 101, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,734
; FILING DATE: 31-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429
; FILING DATE: 22-SEP-1994
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH194-07A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

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## US-08-742-185-101

Query Match 2.0%; Score 103; DB 3; Length 43795;  
Best Local Similarity 100.0%; Pred. No. 3.3e-31; Mismatches 0; Indels 0; Gaps 0;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4955 CCCTGTAATCCAGCAGCTTTGGGAGGCTGAGGCAGGTGATCAGAGTCAAGGATCGA 5014  
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Db 4388 CCCTGTAATCCAGCAGCTTTGGGAGGCTGAGGCAGGTGATCAGAGTCAAGGATCGA 4329  
|||||

Qy 5015 GACCATCTGCTAACACGGTGAACCCCGTCTCTACTAAAAA 5057  
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Db 4328 GACCATCTGCTAACACGGTGAACCCCGTCTCTACTAAAAA 4286  
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## RESULT 9

US-09-128-155-16/c  
; Sequence 16, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128.155  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 60/091.650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054.646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 152331  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(152331)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-16

Query Match 1.6%; Score 83; DB 3; Length 152331;  
Best Local Similarity 100.0%; Pred. No. 1.5e-23;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1567 CCTGATTGAATGTGTGATGTAAGTCACTTTAACTAATCAGGATTAATCCATTAGCAT 1626  
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Db 23907 CCTGATTGAATGTGTGATGTAAGTCACTTTAACTAATCAGGATTAATCCATTAGCAT 23848  
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Qy 1627 TTGCTACCAAGTAGGAAAAAAA 1649  
|||||  
Db 23847 TTGCTACCAAGTAGGAAAAAAA 23825  
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## RESULT 10

US-09-334-601-5/c  
; Sequence 5, Application US/09334601  
; Patent No. 6280989  
; GENERAL INFORMATION:  
; APPLICANT: Kapitonov, Dmitri  
; APPLICANT: Yu, Robert  
; TITLE OF INVENTION: NOVEL STIALYLTRANSFERASES  
; FILE REFERENCE: VCUIP-6  
; CURRENT APPLICATION NUMBER: US/09/334.601  
; CURRENT FILING DATE: 1999-06-17  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 3494  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-334-601-5

Query Match 1.5%; Score 81; DB 4; Length 3494;  
Best Local Similarity 100.0%; Pred. No. 1.5e-22;  
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5089 CCTGTAGTCCAGCTACTCGGAGGCTGAGGCAGGAGAAATGTTGAACCCGGGAGGCAG 5148  
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Db 88 CCTGTAGTCCAGCTACTCGGAGGCTGAGGCAGGAGAAATGTTGAACCCGGGAGGCAG 29  
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Qy 5149 AGCTTGCAGTCAGCCGAGATC 5169  
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Db 28 AGCTTGCAGTCAGCCGAGATC 8  
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## RESULT 11

US-09-740-035-3  
; Sequence 3, Application US/09740035  
; Patent No. 6344353  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001058  
; CURRENT APPLICATION NUMBER: US/09/740.035  
; CURRENT FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 19736  
; TYPE: DNA  
; ORGANISM: Human  
US-09-740-035-3

Query Match 1.4%; Score 74; DB 4; Length 19736;  
Best Local Similarity 100.0%; Pred. No. 6.2e-20;  
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5066 TTAGCCGGCGTGTGGCGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGAGGCAG 5125  
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Db 13951 TTAGCCGGCGTGTGGCGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGAGGCAG 14010  
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Qy 5126 AATGGTGTGAACCC 5139  
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Db 14011 AATGGTGTGAACCC 14024  
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## RESULT 12

US-07-869-933-31  
; Sequence 31, Application US/07869933  
; Patent No. 5770396  
; GENERAL INFORMATION:  
; APPLICANT: KINET, Jean-Pierre  
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
; TITLE OF INVENTION: IMMUNOGLOBULIN  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/869,933  
; FILING DATE: 19920416  
; CLASSIFICATION: 514

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; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11298 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; STRAIN: FcRI beta
; US-07-869-933-31

Query Match 1.3%; Score 70; DB 1; Length 11298;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10775 GGTGGATCAGGAGTCAGAGATCGAGACCATCCTGGCTAAACACGGTGAAACCCCGTCTC 10834

QY 5049 TACTAAAAA 5058
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Db 10835 TACTAAAAA 10844

RESULT 13
US-08-201-879A-2
; Sequence 2, Application US/08201879A
; Patent No. 5807988
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; APPLICANT: JOUVIN, Marie-Helene
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,879A
; FILING DATE: 24-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/869,933
; FILING DATE: 16-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03419
; FILING DATE: 16-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/234/NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11298 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: FcRI beta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(456..511, 1381..1510, 2026..2160, 4475..4531,
; LOCATION: 5079..5237, 5640..5738, 7224..7319)
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Query Match 1.3%; Score 70; DB 1; Length 11298;
Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5049 TACTAAAAA 5058
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RESULT 14
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; Sequence 31, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 11298
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-103-663-31

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Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10775 GGTGGATCAGGAGTCAGAGATCGAGACCATCCTGGCTAAACACGGTGAAACCCCGTCTC 10834

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Db 10835 TACTAAAAA 10844

RESULT 15
US-08-520-373D-4
; Sequence 4, Application US/08520373D
; Patent No. 6451763
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
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; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
; FILE REFERENCE: 2026-4203US1
; CURRENT APPLICATION NUMBER: US/08/520,373D
; CURRENT FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,979
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/894,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 14581
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: mRNA: 6683; EXON: 6683-6790; EXON 11584-11675;
; OTHER INFORMATION: EXON: 14539-14581; INTRON: 6791-11583; INTRON:
; OTHER INFORMATION: 11676-14538; CDS: 11584-11675; 14539-14580
US-08-520-373D-4

Query Match 1.3%; Score 69; DB 4; Length 14581;
Best Local Similarity 100.0%; Pred. No. 5.6e-18;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12885 GGTGGATCAGGAGTCAGGAGATCGAGACCATCTGGCTAACACGGTGAACCCCGTCTC 12944
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QY 5049 TACTAAAAA 5057
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Search completed: November 10, 2002, 04:46:12
Job time : 1269 secs

GenCore version 5.1.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 00:05:56 ; Search time 164 Seconds  
(without alignments)  
11318.521 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	85	1.6	53542	10	US-09-801-574-61
C 6	78	1.5	302250	10	US-09-962-832-154
C 7	77	1.5	203654	10	US-09-820-905-3
C 8	76	1.5	401	10	US-09-795-668-421
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13	72	1.4	30420	10	US-09-764-877-2432
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15	70	1.3	281	10	US-09-764-887-643
16	69	1.3	226	10	US-09-764-869-1423
17	69	1.3	292	10	US-09-764-847-1844
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C 19	69	1.3	342	10	US-09-867-701-8277

20	69	1.3	739	10	US-09-764-877-3833	Sequence 3833, Ap
C 21	69	1.3	1400	10	US-09-263-959-295	Sequence 295, App
22	69	1.3	1408	10	US-09-764-869-1489	Sequence 1489, Ap
23	69	1.3	4978	10	US-09-764-887-355	Sequence 355, App
C 24	69	1.3	6186	10	US-09-764-860-1075	Sequence 1075, Ap
C 25	69	1.3	9745	10	US-09-764-869-2259	Sequence 2259, Ap
C 26	69	1.3	12149	10	US-09-764-869-2258	Sequence 2258, Ap
C 27	69	1.3	15070	10	US-09-764-877-3979	Sequence 3979, Ap
C 28	69	1.3	15071	10	US-09-764-877-3978	Sequence 3978, Ap
C 29	69	1.3	18000	10	US-09-800-631-17	Sequence 17, Appl
C 30	69	1.3	18385	10	US-09-764-860-1018	Sequence 1018, Ap
C 31	69	1.3	22484	10	US-09-875-114-2	Sequence 2, Appli
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C 33	69	1.3	43058	10	US-09-954-456-292	Sequence 292, App
C 34	69	1.3	43058	10	US-09-954-456-529	Sequence 529, App
C 35	69	1.3	43058	10	US-09-880-107-3950	Sequence 3950, Ap
C 36	69	1.3	52216	10	US-09-747-810-1	Sequence 1, Appli
C 37	69	1.3	110096	10	US-09-880-107-1542	Sequence 1542, Ap
C 38	69	1.3	116592	10	US-09-818-512-3	Sequence 3, Appli
C 39	69	1.3	684973	10	US-09-263-959-1	Sequence 1, Appli
C 40	68	1.3	463	10	US-09-764-887-112	Sequence 112, App
41	68	1.3	32195	10	US-09-764-870-611	Sequence 611, App
42	68	1.3	32195	10	US-09-764-870-617	Sequence 617, App
43	68	1.3	32195	10	US-09-764-869-1605	Sequence 1605, Ap
C 44	68	1.3	174493	10	US-09-804-471A-3	Sequence 3, Appli
C 45	67	1.3	26048	10	US-09-764-869-1556	Sequence 1556, Ap

ALIGNMENTS

RESULT 1  
US-09-974-592-3  
; Sequence 3, Application US/09974592  
; Patent No. US20020120121A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; FILE REFERENCE: 07891/009004  
; CURRENT APPLICATION NUMBER: US/09/974,592  
; CURRENT FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US 09/617,053  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800,929  
; PRIOR FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 5232  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: 4623  
; OTHER INFORMATION: n can be any nucleotide  
; NAME/KEY: variation  
; LOCATION: 4622  
; OTHER INFORMATION: n can be any nucleotide  
US-09-974-592-3  
Query Match 100.0%; Score 5232; DB 10; Length 5232;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB	2521	GGCAGTTAAACCTTTTGGTGGCCAATGTGAAATGTAAATGATTTTTATGTTTTTCCCTGCTT	2580
QY	2581	TGTGGATGAAAATATATTTCTGAGTGGTAGTTTTTTTTCACAGGTAGACCACTGCTTATCTTG	2640
DB	2581	TGTGGATGAAAATATATTTCTGAGTGGTAGTTTTTTTTCACAGGTAGACCACTGCTTATCTTG	2640
QY	2641	TTTCAAATTAAGTATTTCTGATTTTCTAAATGAAATATAAATATGTCACAGATCTTCC	2700
DB	2641	TTTCAAATTAAGTATTTCTGATTTTCTAAATGAAATATAAATATGTCACAGATCTTCC	2700
QY	2701	AATTAATTAGTAAAGATTCACTCCTTAATCCTTGCCTAGTTTAAAGCCTGCCTAAGTCACCTT	2760
DB	2701	AATTAATTAGTAAAGATTCACTCCTTAATCCTTGCCTAGTTTAAAGCCTGCCTAAGTCACCTT	2760
QY	2761	ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGTAAAGT	2820
DB	2761	ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGTAAAGT	2820
QY	2821	AGAAGCATGTTGTACACTGCTGTAGTTATAGTCACAGCTTTCCATGTCAGATTCCTCA	2880
DB	2821	AGAAGCATGTTGTACACTGCTGTAGTTATAGTCACAGCTTTCCATGTCAGATTCCTCA	2880
QY	2881	TATCATCTGTATCTTAAAGTTTCATGTCAGTTTTTACCGTTAGGATGATTTAAGATGTAT	2940
DB	2881	TATCATCTGTATCTTAAAGTTTCATGTCAGTTTTTACCGTTAGGATGATTTAAGATGTAT	2940
QY	2941	ATAGACAAAATGTTAAGTCTTCCCTCACTACATATTTTGTGTTTCTTGCGCTAGTAAATAGTA	3000
DB	2941	ATAGACAAAATGTTAAGTCTTCCCTCACTACATATTTTGTGTTTCTTGCGCTAGTAAATAGTA	3000
QY	3001	CTAGATACCTCTGAAATAAATGTCTCTCAAGATCCTTAAACCTCTGGAAATTTATAA	3060
DB	3001	CTAGATACCTCTGAAATAAATGTCTCTCAAGATCCTTAAACCTCTGGAAATTTATAA	3060
QY	3061	AATATTGGCAAGAAAAGAAATAGTGTGTTTAAATATTTTTTAAAAAACACTCTGAATAAG	3120
DB	3061	AATATTGGCAAGAAAAGAAATAGTGTGTTTAAATATTTTTTAAAAAACACTCTGAATAAG	3120
QY	3121	AATCAGTAGGGTATAACTAGAAAGTTTAAAAATGCCTCATAGAAGCTCCAGGGTTTACAT	3180
DB	3121	AATCAGTAGGGTATAACTAGAAAGTTTAAAAATGCCTCATAGAAGCTCCAGGGTTTACAT	3180
QY	3181	TACAGATTTCTCACAAACCAACCATTTGTAGAGGTGAGTAAAGCATGTTACTACAGAGGAA	3240
DB	3181	TACAGATTTCTCACAAACCAACCATTTGTAGAGGTGAGTAAAGCATGTTACTACAGAGGAA	3240
QY	3241	AGTTTGAAGTAAACCTGTAAAAAATATATTTTTTGTGTTACTTTCTAAGAGAAGAGTA	3300
DB	3241	AGTTTGAAGTAAACCTGTAAAAAATATATTTTTTGTGTTACTTTCTAAGAGAAGAGTA	3300
QY	3301	TTGTTATGTCTCCTCAACTCTGTTGATTTACTTACTTAAAGTCATATTCATTTAAACACTT	3360

[illegible]

Db	4381	CAAGTCACCACTTATTTTACATCTTTAGTCATCGCAAGATTCCAAGTAGTTGTTGGCAATAGT	4440
Qy	4441	ACTTATCTTTATTTGTPAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTAATTTTGTAG	4500
Db	4441	ACTTATCTTTATTTGTPAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTAATTTTGTAG	4500
Qy	4501	AAC TGTTTTAGCATTTACAAACTAAATTCAGTTTAATTAATTAAGCTTTATATTGGC	4560
Db	4501	AAC TGTTTTAGCATTTACAAACTAAATTCAGTTTAATTAATTAAGCTTTATATTGGC	4560
Qy	4561	TTTCCCTGCTACATTTGGTTTTTTTCCCTTGCTCCCTTTGATTACGGGCTAAGGTAGGGTAAG	4620
Db	4561	TTTCCCTGCTACATTTGGTTTTTTTCCCTTGCTCCCTTTGATTACGGGCTAAGGTAGGGTAAG	4620
Qy	4621	ANNGGGTAGTGAGGTATATAATGTGATTTGGCCCTGTGTTATTAATGATATTTTGTATT	4680
Db	4621	ANNGGGTAGTGAGGTATATAATGTGATTTGGCCCTGTGTTATTAATGATATTTTGTATT	4680
Qy	4681	TTTTTGTTGTATATATTTACATTTTCAGTAGTTGTTTTTGTGTTTTCCATTTTAGGGGAT	4740
Db	4681	TTTTTGTTGTATATATTTACATTTTCAGTAGTTGTTTTTGTGTTTTCCATTTTAGGGGAT	4740
Qy	4741	AAAAATTTGATTTTGAACATCATGAATGGAGACTACCGCCCCAGCAATTAGTTTTCACATGATA	4800
Db	4741	AAAAATTTGATTTTGAACATCATGAATGGAGACTACCGCCCCAGCAATTAGTTTTCACATGATA	4800
Qy	4801	TACCCCTTTAAACCCGAATCATTTGTTTTATTTCTCGATTACACAGGTGTTGAATGGGGAAA	4860
Db	4801	TACCCCTTTAAACCCGAATCATTTGTTTTATTTCTCGATTACACAGGTGTTGAATGGGGAAA	4860
Qy	4861	GGGGCTAGTATATACGTAGGATATACTATGGAGTATATATATCATTTGCTGTTTAGAGAA	4920
Db	4861	GGGGCTAGTATATACGTAGGATATACTATGGAGTATATATATCATTTGCTGTTTAGAGAA	4920
Qy	4921	ATGAATAAAATGGGGCTGGGCTCAGTGGCTACGCCCTGTAATCCCAGCACTTTTGGGAGG	4980
Db	4921	ATGAATAAAATGGGGCTGGGCTCAGTGGCTCAGGCCCTGTAATCCCAGCACTTTTGGGAGG	4980
Qy	4981	CTGAGCAGGTGGATCACCAGCTCAGGAGATCGAGACCATCCTGGCTTAACACCGTGAAC	5040
Db	4981	CTGAGCAGGTGGATCACCAGGTGAGGAGATCGAGACCATCCTGGCTTAACACCGTGAAC	5040
Qy	5041	CCCGTCTCTACTAAAAACAGAAAATTAGCCGGGCGTGGTGCGGGGGCCCTGTAGTCCCA	5100
Db	5041	CCCGTCTCTACTAAAAACAGAAAATTAGCCGGGCGTGGTGCGGGGGCCCTGTAGTCCCA	5100
Qy	5101	GCTACTCGGGAGGCTGAGCGCAGAGAAATGGTGTAACCCGGGAGGCAGAGCTTGCAGTGA	5160
Db	5101	GCTACTCGGGAGGCTGAGCGCAGAGAAATGGTGTAACCCGGGAGGCAGAGCTTGCAGTGA	5160
Qy	5161	GCCGAGATCTCGGCACCTGCACCTCCAGCCTGGGCAACAGAGCAAGACACTCTGTCTCAAAAA	5220
Db	5161	GCCGAGATCTCGGCACCTGCACCTCCAGCCTGGGCAACAGAGCAAGACACTCTGTCTCAAAAA	5220
Qy	5221	AAAAAANAAG 5232	
Db	5221	AAAAAANAAG 5232	

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RESULT 2
US-09-864-761-13853/c
; Sequence 13853, Application US/098664761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23

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? PRIOR APPLICATION NUMBER: US 60/180,312
? PRIOR FILING DATE: 2000-02-04
? PRIOR APPLICATION NUMBER: US 60/207,456
? PRIOR FILING DATE: 2000-05-26
? PRIOR APPLICATION NUMBER: US 09/632,366
? PRIOR FILING DATE: 2000-08-03
? PRIOR APPLICATION NUMBER: GB 24263.6
? PRIOR FILING DATE: 2000-10-04
? PRIOR APPLICATION NUMBER: US 60/236,359
? PRIOR FILING DATE: 2000-09-27
? PRIOR APPLICATION NUMBER: PCT/US01/006666
? PRIOR FILING DATE: 2001-01-30
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? PRIOR APPLICATION NUMBER: PCT/US01/006664
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/006669
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/006665
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/006668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/006663
? PRIOR FILING DATE: 2001-01-30
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? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 09/608,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
? SEQ ID NO 13853
? LENGTH: 489
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AL022156.1
? OTHER INFORMATION: EXPRESSED IN HB1100, SIGNAL = 1.1
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
? OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
? US-09-864-761-13853

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1







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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-686-421

Query Match      1.5%; Score 76; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4983 GAGCAGGTGGATCACGAGGTCAGGAGTCAGACCATCCTGGCTAACACGCGTGAACCC 5042
|||||
Db 129 GAGCAGGTGGATCACGAGGTCAGGAGTCAGACCATCCTGGCTAACACGCGTGAACCC 70
|||||

Qy 5043 CGTCTCTACTAAAAA 5058
|||||
Db 69 CGTCTCTACTAAAAA 54
|||||

RESULT 10
US-10-014-502-3
; Sequence 3, Application US/10014502
; Patent No. US20020137184A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: US/01058DIV
; CURRENT APPLICATION NUMBER: US/10/014,502
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 09/740,035
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 19736
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-014-502-3

Query Match      1.4%; Score 74; DB 12; Length 19736;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5066 TTACCGCGCGGTGGTGGCGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCGAGG 5125
|||||
Db 13951 TTACCGCGCGGTGGTGGCGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCGAGG 14010
|||||

Qy 5126 AATGGTGTGAACCC 5139
|||||
Db 14011 AATGGTGTGAACCC 14024
|||||

RESULT 11
US-09-795-668-1/c
; Sequence 1, Application US/0979568
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/795,686
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r=g or a
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y=t/u or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m=a or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k=g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s=g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w=a or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: b=g or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d=a or g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h=a or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v=a or g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or g or c or t/u
US-09-795-668-1

Query Match      1.4%; Score 73; DB 10; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 9.1e-17;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5089 CCTGTAGTCCCGAGCTACTCGGGAGGCTGAGGAGGAGATGGTGAACCCGGGAGGCGAG 5148
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Db 1501676 CCTGTAGTCCCGAGCTACTCGGGAGGCTGAGGAGGAGATGGTGAACCCGGGAGGCGAG 1501617
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Qy 5149 AGCTTGCAGTGAG 5161
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Db 1501616 AGCTTGCAGTGAG 1501604
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RESULT 12
US-09-795-686-1/c
; Sequence 1, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r=g or a
; NAME/KEY: misc_feature
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; OTHER INFORMATION: y=t/u or c
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m=a or c
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k=g or t/u
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s=g or c
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w=a or t/u
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: b=g or c or t/u
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d=a or g or t/u
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h=a or c or t/u
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v=a or g or c
; NAME/KEY: misc.feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or g or c or t/u
US-09-795-686-1

Query Match      1.4%; Score 73; DB 10; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 9.1e-17;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5089 CCTGTAGTCCAGCTACTCGGAGGCTGAGCGAGGAGATGGTGTGAACCCGGGAGGCAG 5148
|||||
Db 1501676 CCTGTAGTCCAGCTACTCGGAGGCTGAGCGAGGAGATGGTGTGAACCCGGGAGGCAG 1501617

QY 5149 AGCTTGCAGTGAG 5161
|||||
Db 1501616 AGCTTGCAGTGAG 1501604

RESULT 13
US-09-764-877-2432
; Sequence 2432, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2432
; LENGTH: 30420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2432

Query Match      1.4%; Score 72; DB 10; Length 30420;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5075 CTGTGTGGCGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGCGAGGAGATGGTGTG 5134
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Db 3832 CTGTGTGGCGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGCGAGGAGATGGTGTG 3891

QY 5135 AACCCGGGAGGC 5146
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Db 3892 AACCCGGGAGGC 3903

RESULT 14
US-09-867-701-7428
; Sequence 7428, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Robert
; APPLICANT: Aglate, Paul A.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7428
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-7428

Query Match      1.4%; Score 71; DB 10; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4956 CCTGTAATCCAGCAGCTTTGGAGGCTGAGCGAGGTGGATCATCAGAGTCAGAGATCGAG 5015
|||||
Db 91 CCTGTAATCCAGCAGCAGCTTTGGAGGCTGAGCGAGGTGGATCATCAGAGTCAGAGATCGAG 150

QY 5016 ACCATCCTGGC 5026
|||||
Db 151 ACCATCCTGGC 161

RESULT 15
US-09-764-887-643
; Sequence 643, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA113
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 643
; LENGTH: 281
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-643

Query Match      1.3%; Score 70; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 148 AGCTACTCGGAGGCTGAGCGAGGAGAAATGGTGTGAACCCGGGAGGAGCTTGCAGTG 207

QY 5160 AGCCGAGATC 5169
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Db 208 AGCCGAGATC 217

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GenCore version 5.1.3  
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Minimum DB seq length: 0  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5232	100.0	5232	36	US-09-974-592-3
2	2511	48.0	8763	1	PCT-US01-01324-3044
3	2511	48.0	8763	39	US-10-079-979-3044
4	2278	43.5	3000	26	US-09-672-717-231
5	2027	38.7	2404	36	US-09-964-899-38
6	1990	38.0	2540	1	PCT-US00-00583-1
7	1990	38.0	2540	1	PCT-US02-11757-25
8	1990	38.0	2540	1	PCT-US02-11758-25
9	1990	38.0	2540	9	US-08-576-956-3
10	1990	38.0	2540	9	US-08-576-956A-3
11	1990	38.0	2540	14	US-09-011-356-3
12	1990	38.0	2540	14	US-09-011-356-3
13	1990	38.0	2540	14	US-09-023-655-900
14	1990	38.0	2540	14	US-09-053-375B-219
15	1990	38.0	2540	16	US-09-201-932-3
16	1990	38.0	2540	16	US-09-201-932-3
17	1990	38.0	2540	16	US-09-201-936-3
18	1990	38.0	2540	25	US-09-654-743-3
19	1990	38.0	2540	26	US-09-672-717-218
20	1990	38.0	2540	38	US-10-007-926A-274
21	1990	38.0	2540	39	US-10-070-789-1



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QY 1201 AAGAAAAATATGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT 1260  
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QY 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320  
Db 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320  
QY 1321 TCATTTACAAAAGAGATTTAGTACTGAAGAGCAGCTAAGGCGCTGCAAGAGGAGAGCTT 1380  
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Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTCTTTAGTTGGCAATATA 1680  
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Db 1681 ATCTTTGAATTTCTGATTTTTCAGGGTATAGCTGTATATCCATTTTTTTTACTGTTA 1740  
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QY 1801 ATTCATAGTATAGTAAATTTCTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1860  
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QY 1921 ATCTCCCAATACATAATTTGTTGTGTAAGGAAATTAATTTGTTCCATGCTGGTG 1980  
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QY 1981 GAAAGATAGAGATTGTTTTAGAGTTGGTTGTTGTTGTTTGGATTCTGTCCATTTTCT 2040  
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QY 2701 AATTAATAGTAGAATTCATCCTTAATCCTGTCTAGTTTAAAGCCTGCCCTAACGTTT 2760  
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Db 2881 TATCATCTTGTATCTTAAAGTTTTCATGAGTTTACCCGTTAGGATGATTAAGATGAT 2940  
QY 2941 ATAGGCAAAATGTTAAGTCTTTCTACCTACATTTGTTTCTGGCTAGTAATAGTA 3000  
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QY 3001 GTAGATCTTCTGAAATAAATGTTTCTCAAGATCCTTAAAGCCTCTTGGAATTTATAA 3060  
Db 3001 GTAGATCTTCTGAAATAAATGTTTCTCAAGATCCTTAAAGCCTCTTGGAATTTATAA 3060  
QY 3061 AATATTGGCAAGAAAAAGAAATAGTTTAAATATTTTTTAAAGCACTTTGAATAAG 3120  
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QY 3301 TTGTTATGTTTCTTCTAACCTTCTGTTGATTTACTTTTAAAGTGAATTTTAAACATT 3360  
Db 3301 TTGTTATGTTTCTTCTAACCTTCTGTTGATTTACTTTTAAAGTGAATTTTAAACATT 3360





Query Match 48.0%; Score 2511; DB 1; Length 8763; Best local similarity 99.8%; Pred. No. 0; Matches 2881; Conservative 0; Mismatches 5; Indels 1; Gaps 1;									
QY	2344	GGGCGCTTTTCACATTTCTACATTTTTCATTTTGTCTGTTCCGAATTTTATAAGTATGTA	2403						
Db	1	GGGCGCTTTTCACATTTCTACATTTTTCATTTTGTCTGTTCCGAATTTTATAAGTATGTA	60						
QY	2404	TTACTTTTGTAAACAGAAATTTTAGAAGATTTTCTCGATTTAAAGGCTTAGGCATGTT	2463						
Db	61	TTACTTTTGTAAACAGAAATTTTAGAAGATTTTCTCGATTTAAAGGCTTAGGCATGTT	120						
QY	2464	CAAAAGCGCTGCAAAACTACATTCACATCAGCTTTAGTTTTCCTAAATCCAAAGAGGAGGG	2523						
Db	121	CAAAAGCGCTGCAAAACTACATTCACATCAGCTTTAGTTTTCCTAAATCCAAAGAGGAGGG	180						
QY	2524	CAGTTAACCTTTTGTGGCCAAATGTGAATGTAAATGATTTATGTGTTTTCCTGCTTTGT	2583						
Db	181	CAGTTAACCTTTTGTGGCCAAATGTGAATGTAAATGATTTATGTGTTTTCCTGCTTTGT	240						
QY	2584	GGATGAAAATATTTCTGAGTGTAGTTTTCGACAGGTAGACCATGCTCTATCTGTTT	2643						
Db	241	GGATGAAAATATTTCTGAGTGTAGTTTTCGACAGGTAGACCATGCTCTATCTGTTT	300						
QY	2644	CAAAATTAAGTATTTCTGATTTTGTAAATGAAATATAAAATATGCTTCAGATCTTCCAAT	2703						
Db	301	CAAAATTAAGTATTTCTGATTTTGTAAATGAAATATAAAATATGCTTCAGATCTTCCAAT	360						
QY	2704	TAATTAGTAAGGATTCATCCTTAATCCTGCTAGTTTAAAGCGCTGACCTTAAGTACT	2763						
Db	361	TAATTAGTAAGGATTCATCCTTAATCCTGCTAGTTTAAAGCGCTGACCTTAAGTACT	420						
QY	2764	AAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGTAAAGTAGA	2823						
Db	421	AAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGTAAAGTAGA	480						
QY	2824	AGCATGTTTGTACACTGTTTGTAGTATATAGTGACAGCTTTTCCATGTTGAGATCTCATAT	2883						
Db	481	AGCATGTTTGTACACTGTTTGTAGTATATAGTGACAGCTTTTCCATGTTGAGATCTCATAT	540						
QY	2884	CATCTTGATCTTAAAGTTTCATGTGAGTTTTCACCGTTAGGATGATTAAGATGTATATA	2943						
Db	541	CATCTTGATCTTAAAGTTTCATGTGAGTTTTCACCGTTAGGATGATTAAGATGTATATA	600						
QY	2944	GGACAAAATGTTAAGCTTTCCCTACCTACATTTGTTTTCCTGGCTAGTAAGTAGTA	3003						
Db	601	GGACAAAATGTTAAGCTTTCCCTACCTACATTTGTTTTCCTGGCTAGTAAGTAGTA	660						
QY	3004	GATACTTCTCAAAATAAATGTTCTCTCAAGATCCTTAAACCTCTTGGAAATTTATAAAAT	3063						
Db	661	GATACTTCTCAAAATAAATGTTCTCTCAAGATCCTTAAACCTCTTGGAAATTTATAAAAT	720						
QY	3064	ATTGGCAAGAAAAGAGAATAGTTGTTTAAATATTTTAAAAAACACTTTGAATAAGAAT	3123						
Db	721	ATTGGCAAGAAAAGAGAATAGTTGTTTAAATATTTTAAAAAACACTTTGAATAAGAAT	780						
QY	3124	CAGTAGGGTATAAATAGATTTTAAATGCGCTCATAGAACGTCGAGGTTTACATTTAC	3183						
Db	781	CAGTAGGGTATAAATAGATTTTAAATGCGCTCATAGAACGTCGAGGTTTACATTTAC	840						
QY	3184	AAGATTTCTCAACAAAACCCATGTTAGAGGTGAGTAAGGATGTTACTACAGAGGAAAGT	3243						
Db	841	AAGATTTCTCAACAAAACCCATGTTAGAGGTGAGTAAGGATGTTACTACAGAGGAAAGT	900						
QY	3244	TTGAGAGTAAACCTGTAAGAAATATATTTTGTGTACTTTCTTAAGAGAAAGAGTATTG	3303						
Db	901	TTGAGAGTAAACCTGTAAGAAATATATTTTGTGTACTTTCTTAAGAGAAAGAGTATTG	960						
QY	3304	TTATGTTCTCCTAACCTGTTGATTTACTACTTTTAAAGTATATTTTAAACATTTGCA	3363						
Db	961	TTATGTTCTCCTAACCTGTTGATTTACTACTTTTAAAGTATATTTTAAACATTTGCA	1020						

QY	3364	AATTTATTTTATTTATTTATTTTCTTTTGTAGATGGAGCTTGTCTGTGTACCCAGGCTG	3423						
Db	1021	AATTTATTTTATTTATTTATTTTCTTTTGTAGATGGAGCTTGTCTGTGTACCCAGGCTG	1080						
QY	3424	GAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCCCTTCTGGGTTCAAGGATTC	3483						
Db	1081	GAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCCCTTCTGGGTTCAAGGATTC	1140						
QY	3484	CGTGCCCTCAGCTTCCCTGAGTAGCTGGAATTTACAGGAGGTGCCACCATGCCCGACTAAT	3543						
Db	1141	CGTGCCCTCAGCTTCCCTGAGTAGCTGGAATTTACAGGAGGTGCCACCATGCCCGACTAAT	1200						
QY	3544	TTTTTTTATTTTATAGTAGACGGGGTTTCCACATGTTGGCCAGGCTGGTATCAAACTCC	3603						
Db	1201	TTTTTTTATTTTATAGTAGACGGGGTTTCCACATGTTGGCCAGGCTGGTATCAAACTCC	1260						
QY	3604	TGACCTCAAGAGATCCACTCGCCTTGCCCTCCCAAAGTGTGGGATTTACAGGCTTGAGCC	3663						
Db	1261	TGACCTCAAGAGATCCACTCGCCTTGCCCTCCCAAAGTGTGGGATTTACAGGCTTGAGCC	1320						
QY	3664	ACCAGCGCCGGCTAAACACATTTGCAAAATTTAAATGAGAGTTTAAATAATTAATGACT	3723						
Db	1321	ACCAGCGCCGGCTAAACACATTTGCAAAATTTAAATGAGAGTTTAAATAATTAATGACT	1380						
QY	3724	GCCTGTTTCTGTTTATAGTATGTAATCCTCAGTCTTTCACCTTTGACACTGTCTGCCACT	3783						
Db	1381	GCCTGTTTCTGTTTATAGTATGTAATCCTCAGTCTTTCACCTTTGACACTGTCTGCCACT	1440						
QY	3784	TAGTTTGGTTATATATAGTCATTAACCTGAAATTTGGTCTGTATAGTCTAGACTTTAAATTTA	3843						
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QY	3904	CACCTTCCAACTCAGGTAGTGTCAATCTAGTTGTTAGTGGTGGTCAAGGACTCAAGGACTGAAT	3963						
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QY	3964	TGTTTTTAAACATAAGGCTTTTCTGTTCTGGAGCGGCACTTCATTAATAATTTCTTCTAAAA	4023						
Db	1621	TGTTTTTAAACATAAGGCTTTTCTGTTCTGGAGCGGCACTTCATTAATAATTTCTTCTAAAA	1680						
QY	4024	CTTGATGTTTATAGGTTAAAGCAAGACTTTTCTCTCTCCATGAGTGTGGAATTTA	4083						
Db	1681	CTTGATGTTTATAGGTTAAAGCAAGACTTTTCTCTCTCCATGAGTGTGGAATTTA	1740						
QY	4084	ATGCACAACGCTGATGTGGCTTAAACAAGTTTATTTTAAAGAAATGTTTAAAGAAATGCTGTTC	4143						
Db	1741	ATGCACAACGCTGATGTGGCTTAAACAAGTTTATTTTAAAGAAATGTTTAAAGAAATGCTGTTC	1800						
QY	4144	TTCAAGTCTTTAAATCACTCAGCAGCTCCAACTTCTAATCAAAATTTTGGAGACTTAACA	4203						
Db	1801	TTCAAGTCTTTAAATCACTCAGCAGCTCCAACTTCTAATCAAAATTTTGGAGACTTAACA	1860						
QY	4204	GCATTTCTGCTGTCTGAACTATAAAGCAGCGGATTTTCCATCTAATTTCCGCAAAA	4263						
Db	1861	GCATTTCTGCTGTCTGAACTATAAAGCAGCGGATTTTCCATCTAATTTCCGCAAAA	1920						
QY	4264	ATTGATCATTTGCAAGCTCAAACTATAGCATATCCAAATCTTTTCCCTCCCAAGAG	4323						
Db	1921	ATTGATCATTTGCAAGCTCAAACTATAGCATATCCAAATCTTTTCCCTCCCAAGAG	1980						
QY	4324	TTCTCAGTGTCTACATGTAGACTTATCTTTTCTGTATAAAGTTTCACTCTAGAGATTTCAA	4383						
Db	1981	TTCTCAGTGTCTACATGTAGACTTATCTTTTCTGTATAAAGTTTCACTCTAGAGATTTCAA	2040						
QY	4384	GTCAACACTTATTTTACATTTTAGTCATGCAAAAGATTTCAAGTAGTTTTTGAATTAAGTACT	4443						
Db	2041	GTCAACACTTATTTTACATTTTAGTCATGCAAAAGATTTCAAGTAGTTTTTGAATTAAGTACT	2100						
QY	4444	TATCTTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTAAATTTTGTAGAAC	4503						



QY 3364 AATTATATTTTATTTATTTTCTTTTGTGAGATGGAGTCTTGCTGTGCACCCAGGCTG 3423  
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Db 1021 AATTTATTTTATTTATTTTCTTTTGTAGATGGAGTCTTGCTGTGCACCCAGGCTG 1080  
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Db 1081 GAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCTTCTGGGTTCAAGCGATTCT 1140  
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QY 3484 CGTGCTCAGCTTCTTGAGTAGTGGAAATTACAGGCAGGTGCCACCATCCCGACTAAATT 3543  
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QY 3604 TGACCTCAAGAGATCCACTCGGCTTGCCCTCCCAAGTCTGGGATTACAGGTTTGAGCC 3663  
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QY 3964 TGTTTTAAATTAAGGCTTTTCTGTTCTGGGAGCCGCACTTCATTAATAATTTCTTAAAA 4023  
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Db 1621 TGTTTTAAATTAAGGCTTTTCTGTTCTGGGAGCCGCACTTCATTAATAATTTCTTAAAA 1680  
|||||  
QY 4024 CTGTATGTTTGAAGTAAGCAAGACTTTTCTTCTCCCTCCATGAGTTGTGAATTTA 4083  
|||||  
Db 1681 CTGTATGTTTGAAGTAAGCAAGACTTTTCTTCTCCCTCCATGAGTTGTGAATTTA 1740  
|||||  
QY 4084 ATGCACAACGCTGATGGCTAACAAAGTTTATTTTAAAGAAATGTTTAAAGAAATGCTGTGC 4143  
|||||  
Db 1741 ATGCACAACGCTGATGGCTAACAAAGTTTATTTTAAAGAAATGTTTAAAGAAATGCTGTGC 1800  
|||||  
QY 4144 TTCAGGTTCTTAAATCACTCAGCACTCCAACTTCTTAATCAAAATTTTGGAGACTTTAAAC 4203  
|||||  
Db 1801 TTCAGGTTCTTAAATCACTCAGCACTCCAACTTCTTAATCAAAATTTTGGAGACTTTAAAC 1860  
|||||  
QY 4204 GCATTTGCTGTGTTGAACATATAAAAGCACCGGATCTTTCCATCTAATCCGCAAA 4263  
|||||  
Db 1861 GCATTTGCTGTGTTGAACATATAAAAGCACCGGATCTTTCCATCTAATCCGCAAA 1920  
|||||  
QY 4264 ATTGATCAATTTGCAAAAGTCAAACTATAGCCATATCAAACTTTTCCCTCCCAAGAG 4323  
|||||  
Db 1921 ATTGATCAATTTGCAAAAGTCAAACTATAGCCATATCAAACTTTTCCCTCCCAAGAG 1980  
|||||  
QY 4324 TTCTCAGTCTACATGTAGACTATTTCTTCTGTATGAAGTTCACTCTAGGATTTCAA 4383  
|||||  
Db 1981 TTCTCAGTCTACATGTAGACTATTTCTTCTGTATGAAGTTCACTCTAGGATTTCAA 2040  
|||||  
QY 4384 GTCACCACTTATTTTACATTTTAGTCATCAAGATTCAGTAGTTTTCATTAAGTACT 4443  
|||||  
Db 2041 GTCACCACTTATTTTACATTTTAGTCATCAAGATTCAGTAGTTTTCATTAAGTACT 2100  
|||||  
QY 4444 TATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTAATTTTGGAGAC 4503  
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Db 2101 TATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTTGCTTAATTTTGGAGAC 2160  
|||||  
QY 4504 TGGTTTTAGCATTTACAAACTAAATTTCCAGTTAAATTAATTAAGCTTTATATTTGCTTTT 4563  
|||||  
Db 2161 TGGTTTTAGCATTTACAAACTAAATTTCCAGTTAAATTAATTAAGCTTTATATTTGCTTTT 2220  
|||||  
QY 4564 CTTGCTACATTTGGTTTTTTTCCCTCTCCCTTTGATTTAGGGCTAAGGTAAGANN 4623  
|||||  
Db 2221 CTTGCTACATTTGGTTTTTTTCCCTCTCCCTTTGATTTAGGGCTAAGGTTAGGT - AGAGT 2279  
|||||  
QY 4624 GGGTGTAGTGTATATAATGTGATTTGGCCCTGTGATTAATGATATTTTGTATTTT 4683  
|||||  
Db 2280 GGGTGTAGTGTATATAATGTGATTTGGCCCTGTGATTAATGATATTTTGTATTTT 2339  
|||||  
QY 4684 TGGTGTATATATTTTACATTTTTCAGTAGTTGTTTTTGTCTTCCATTTTAGGGGATAA 4743  
|||||  
Db 2340 TGGTGTATATATTTTACATTTTTCAGTAGTTGTTTTTGTCTTCCATTTTAGTGSATAA 2399  
|||||  
QY 4744 ATTTGTATTTTGAACATGATGAATGGAGACTACCGCCCGCAGCATTTGATTCACATGATATAC 4803  
|||||  
Db 2400 ATTTGTATTTTGAACATGATGAATGGAGACTACCGCCCGCAGCATTTGATTCACATGATATAC 2459  
|||||  
QY 4804 CCTTTAAACCCGAATCATTTGTTTTTATTTCTGATTACACAGGTGTTGAATGGGGAAGGG 4863  
|||||  
Db 2460 CCTTTAAACCCGAATCATTTGTTTTTATTTCTGATTACACAGGTGTTGAATGGGGAAGGG 2519  
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QY 4864 GCTAGTATATCAGTAGGATATACTATGGGATGTATATATATCATTTGCTGTAGAGAAATG 4923  
|||||  
Db 2520 GCTAGTATATCAGTAGGATATACTATGGGATGTATATATATCATTTGCTGTAGAGAAATG 2579  
|||||  
QY 4924 AAATAAATGGGCTGGGCTCAGTGGCTCAGGCTCTCAAGCTCTTAATCCCGACACTTTGGGAGGCTG 4983  
|||||  
Db 2580 AAATAAATGGGCTGGGCTCAGTGGCTCAGGCTCTCAAGCTCTTAATCCCGACACTTTGGGAGGCTG 2639  
|||||  
QY 4984 AGSCAGGTGGATCACAGGTCAGGAGTCAAGGATCGAGACCATCTCTGGCTAAACCGGTGAACCC 5043  
|||||  
Db 2640 AGSCAGGTGGATCACAGGTCAGGAGTCAAGGATCGAGACCATCTCTGGCTAAACCGGTGAACCC 2699  
|||||  
QY 5044 GTCCTCTACTAAAAACAGAAAAATTTAGCCGGGCTGTGGGGGGGCTGTAGTCCAGCT 5103  
|||||  
Db 2700 GTCCTCTACTAAAAACAGAAAAATTTAGCCGGGCTGTGGGGGGGCTGTAGTCCAGCT 2759  
|||||  
QY 5104 ACTCGGAGGCTGAGGAGGAGAAATGTTGTAACCCGGGAGGAGAGCTTGCAGTGAGCC 5163  
|||||  
Db 2760 ACTCGGAGGCTGAGGAGGAGAAATGTTGTAACCCGGGAGGAGAGCTTGCAGTGAGCC 2819  
|||||  
QY 5164 GAGATCTGCCACTGCATCCAGCTCCAGCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAAA 5223  
|||||  
Db 2820 GAGATCTGCCACTGCATCCAGCTCCAGCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAAAA 2879  
|||||  
QY 5224 AAAAAA 5230  
|||||  
Db 2880 AAAAAA 2886  
|||||

RESULT 4  
US-09-672-717-231  
; Sequence 231, Application US/09672717  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: LaCasse, Eric  
; APPLICANT: Baird, Stephen  
; APPLICANT: Holcik, Martin  
; APPLICANT: Young, Sean  
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses  
; TITLE OF INVENTION: Thereof  
; FILE REFERENCE: 07891/025001  
; CURRENT APPLICATION NUMBER: US/09/672,717  
; CURRENT FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 231

; LENGTH: 3000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-672-717-231

Query Match 43.5%; Score 2278; DB 26; Length 3000;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGTGGCAAGTCTCTATTTTCAAGAGAAGATGACTTTTAAACAGTCTTTTGAAGGATCT 60  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
657 GAAAGGTGGCAAGTCTCTATTTTCAAGAGAAGATGACTTTTAAACAGTCTTTTGAAGGATCT 716  
QY 61 AAAACTTGTGTACCTGACACATCAATAGGAAGAAGATTTGTAGAGAGTTTAAATAGA 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
717 AAAACTTGTGTACCTGACACATCAATAGGAAGAAGATTTGTAGAGAGTTTAAATAGA 776  
QY 121 TTAANAACCTTTTGTCTAATTTTCAAGTGGTAGTCTCTTTCAGCATCAACACTGGCAGCA 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
777 TTAANAACCTTTTGTCTAATTTTCAAGTGGTAGTCTCTTTCAGCATCAACACTGGCAGCA 836  
QY 181 GCAGGGTTTCTTTATCTGTTGAAGGAGATACCGTGGGTGCTTTAGTTGTCTATGTCAGCT 240  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
837 GCAGGGTTTCTTTATCTGTTGAAGGAGATACCGTGGGTGCTTTAGTTGTCTATGTCAGCT 896  
QY 241 GTAGATAGTGGCAATATGGAGACTCAGCAGTTTGGAAAGACACAGGAAGTATCCCCAAAT 300  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
897 GTAGATAGTGGCAATATGGAGACTCAGCAGTTTGGAAAGACACAGGAAGTATCCCCAAAT 956  
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAANAATAGTCCAGCGAGTCTACAAATTCGGT 360  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
957 TGCAGATTTATCAACGGCTTTTATCTTGAANAATAGTCCAGCGAGTCTACAAATTCGGT 1016  
QY 361 ATCCAGAAATGTCAGTACAAAGTTGAAACTATCTGGAAGCAGAGATCATTTTGCCTTA 420  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1017 ATCCAGAAATGTCAGTACAAAGTTGAAACTATCTGGAAGCAGAGATCATTTTGCCTTA 1076  
QY 421 GACAGGCCATCTGAGACACATGACAGTATCTTTTGAAGTGGCAGGTTGTAGATATA 480  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1077 GACAGGCCATCTGAGACACATGACAGTATCTTTTGAAGTGGCAGGTTGTAGATATA 1136  
QY 481 TCAGACACCATATACCGGAGGAACCTTGCATGTATAGTGAAGAGCTAGATTAAGTCC 540  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1137 TCAGACACCATATACCGGAGGAACCTTGCATGTATAGTGAAGAGCTAGATTAAGTCC 1196  
QY 541 TTTCCAGAACTGGCCAGACTATGCTACACTAACCCCAAGAGAGTTAGCAAGTGTGGACTC 600  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1197 TTTCCAGAACTGGCCAGACTATGCTACACTAACCCCAAGAGAGTTAGCAAGTGTGGACTC 1256  
QY 601 TACTACAGAGTATGTTGACCAAGTGCAGTGTCTTGTGTGGTGGAAACTGAAAAAT 660  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1257 TACTACAGAGTATGTTGACCAAGTGCAGTGTCTTGTGTGGTGGAAACTGAAAAAT 1316  
QY 661 TGGGAACCTTGTGATCGCTGCTCAGACACAGGCGACACTTTTCCATTTGCTTCTTT 720  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1317 TGGGAACCTTGTGATCGCTGCTCAGACACAGGCGACACTTTTCCATTTGCTTCTTT 1376  
QY 721 GTTTTGGCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGTGAGTCTGTAGAGAAAT 780  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1377 GTTTTGGCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGTGAGTCTGTAGAGAAAT 1436  
QY 781 TTCCCAATTCACAAATCTTCCAGAAATCCATCCATGCGCAGATTTAGAGCACGGATC 840  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1437 TTCCCAATTCACAAATCTTCCAGAAATCCATCCATGCGCAGATTTAGAGCACGGATC 1496  
QY 841 TTTTACTTTTGGGACATGGATATCTCAGTTTAAAGAGAGAGCTTGAAGAGCTGGATTT 900  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1497 TTTTACTTTTGGGACATGGATATCTCAGTTTAAAGAGAGAGCTTGAAGAGCTGGATTT 1556  
QY 901 TATGCTTTAGGTGAAGTGAATAAGTAAAGTGTCTTTCACCTGTGGAGGAGGCTTAACATGAT 960  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1557 TATGCTTTAGGTGAAGTGAATAAGTAAAGTGTCTTTCACCTGTGGAGGAGGCTTAACATGAT 1616

QY 961 TGGAGCCCACTGAGACACCCTTGGGAACAACATGCTAAATGGTATATCCAGGGTGCATAATAT 1020  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1617 TGGAGCCCACTGAGACACCCTTGGGAACAACATGCTAAATGGTATATCCAGGGTGCATAATAT 1676  
QY 1021 CTGTTAGAACAGAGGACAGCAAGATATATAAACAATATTCATTTAACTCACTCACTTGAAG 1080  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1677 CTGTTAGAACAGAGGACAGCAAGATATATAAACAATATTCATTTAACTCACTCACTTGAAG 1736  
QY 1081 GAGTGTCTGCTAAGAACTACTGAGAAAACACCACATCACTAACTAGAGAATTTGATGATACC 1140  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1737 GAGTGTCTGCTAAGAACTACTGAGAAAACACCACATCACTAACTAGAGAATTTGATGATACC 1796  
QY 1141 ATCTTCCAAATCTCTGTTGACAGAGCTATACGAATGGGGTTCAGTTTCAAGGACATTT 1200  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1797 ATCTTCCAAATCTCTGTTGACAGAGCTATACGAATGGGGTTCAGTTTCAAGGACATTT 1856  
QY 1201 AAGAAAATAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT 1260  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1857 AAGAAAATAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGGTT 1916  
QY 1261 CTGTTTCAGATCTAGTGAATGCTCAGAAAACAGAGTATGCAAGATGAGTCAAGTCAAGCT 1320  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1917 CTGTTTCAGATCTAGTGAATGCTCAGAAAACAGAGTATGCAAGATGAGTCAAGTCAAGCT 1976  
QY 1321 TCATTACAGAAAGAGATTTAGTCTGAAAGAGAGCTAAAGGCGCTGCAAGAGGAGAAAGCTT 1380  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1977 TCATTACAGAAAGAGATTTAGTCTGAAAGAGAGCTAAAGGCGCTGCAAGAGGAGAAAGCTT 2036  
QY 1381 TGCAAAATCTGTATGGATAGAAATATTCGTTATCGTTTTTGTCTCTTGGACATCTAGTC 1440  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2037 TGCAAAATCTGTATGGATAGAAATATTCGTTATCGTTTTTGTCTCTTGGACATCTAGTC 2096  
QY 1441 ACTTGTAAACAATGCTGTGAAGCAGTTTGACAAGTGTCCCATGTCTACACAGTCACTACT 1500  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2097 ACTTGTAAACAATGCTGTGAAGCAGTTTGACAAGTGTCCCATGTCTACACAGTCACTACT 2156  
QY 1501 TTCAGCAAAAATTTTATGCTCTTAATCTAACTCTATAGTAGGCACTGTTTANGTGTGTTCT 1560  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2157 TTCAGCAAAAATTTTATGCTCTTAATCTAACTCTATAGTAGGCACTGTTTANGTGTGTTCT 2216  
QY 1561 TATTACCTCTGATGAATGCTGTGATGCAACTGACTTTAAAGTAAATCAGGATTTGAATTCAT 1620  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2217 TATTACCTCTGATGAATGCTGTGATGCAACTGACTTTAAAGTAAATCAGGATTTGAATTCAT 2276  
QY 1621 TAGCATTTGCTTACCAAGTAGGAAAAAATGTCATGCGAGTGTGTTTGTAGTTGGCAATATA 1680  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2277 TAGCATTTGCTTACCAAGTAGGAAAAAATGTCATGCGAGTGTGTTTGTAGTTGGCAATATA 2336  
QY 1681 ATCTTTGAAATTTCTGATTTTTCAGGGTATTTAGCTGTATTTATCCATTTTTTTTACTGTTA 1740  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2337 ATCTTTGAAATTTCTGATTTTTCAGGGTATTTAGCTGTATTTATCCATTTTTTTTACTGTTA 2396  
QY 1741 TTTAATTTGAACCATAGACTAAGAAATTAAGAGCATCATCTATTAACCTGAACACAAATGTT 1800  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2397 TTTAATTTGAACCATAGACTAAGAAATTAAGAGCATCATCTATTAACCTGAACACAAATGTT 2456  
QY 1801 ATTCATAGTACTGATTTTAAATTTCTAAGTGAAGTAAATTAATCACTGAGATTTTAT 1860  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2457 ATTCATAGTACTGATTTTAAATTTCTAAGTGAAGTAAATTAATCACTGAGATTTTAT 2516  
QY 1861 TCTTTTCAGATAGCTTTAAACAATGGAGCTTTCGTATATAAATGTCGAGATTTAGAGTTA 1920  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2517 TCTTTTCAGATAGCTTTAAACAATGGAGCTTTCGTATATAAATGTCGAGATTTAGAGTTA 2576  
QY 1921 ATCTCCCCAATCACTAATTTTGTCTGTAAGAAAGAAATTAATTTCCATCTCTGTTG 1980  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2577 ATCTCCCCAATCACTAATTTTGTCTGTAAGAAAGAAATTAATTTCCATCTCTGTTG 2636  
QY 1981 GAAAGATAGAGATTTGTTTGTAGAGTTGGTGTGTTTGTAGGATTTCTGTGCCATTTTCT 2040  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2637 GAAAGATAGAGATTTGTTTGTAGAGTTGGTGTGTTTGTAGGATTTCTGTGCCATTTTCT 2696  
QY 2041 TTTAAGCTTTAAACACAGTACTTGTGCGAATTTATTTTTTAAAGTGAATTTGCCATTTTG 2100







Db 901 |||||TATGCTTAAAGTGAAGTAAAGTCTTCACTGTGGAGGGCTAACTGAT 960  
Qy 961 TGGAGCCAGTGAAGCCCTTGGCAACAACATGTAATGCTATCCAGGGTGCATAAT 1020  
Db 961 TGGAGCCAGTGAAGCCCTTGGCAACAACATGTAATGCTATCCAGGGTGCATAAT 1020  
Qy 1021 CTGTTAGAACAGAGGACAGAATATATAACAATATTCATTAACTCACTTCTGAG 1080  
Db 1021 CTGTTAGAACAGAGGACAGAATATATAACAATATTCATTAACTCACTTCTGAG 1080  
Qy 1081 GAGTGTCTGTTAGAACTCTGAGAAAACACCATCACTAAGTAAGTAATGATATACC 1140  
Db 1081 GAGTGTCTGTTAGAACTCTGAGAAAACACCATCACTAAGTAAGTAATGATATACC 1140  
Qy 1141 ATCTTCCAAAATCCCTATGTTACAGAAGCTATACCAATGGGGTTCAGTTTCAAGGACATT 1200  
Db 1141 ATCTTCCAAAATCCCTATGTTACAGAAGCTATACCAATGGGGTTCAGTTTCAAGGACATT 1200  
Qy 1201 AAGAAAATTAATGGAGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAAGTT 1260  
Db 1201 AAGAAAATTAATGGAGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAAGTT 1260  
Qy 1261 CTGGTTGAGATCTAGTGAATGCTCAGAAAACAGATATGCAAGATGAGTCAAGTCAAGT 1320  
Db 1261 CTGGTTGAGATCTAGTGAATGCTCAGAAAACAGATATGCAAGATGAGTCAAGTCAAGT 1320  
Qy 1321 TCATTACAGAAAGATAGTACTCAAGAGCAGCTAAAGCGCTCAGAGGAGAGGCTT 1380  
Db 1321 TCATTACAGAAAGATAGTACTCAAGAGCAGCTAAAGCGCTCAGAGGAGAGGCTT 1380  
Qy 1381 TGCAAAATCTGTTAGTAAATATGCTATCGTTTTTGTTCCTGTGGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGTTAGTAAATATGCTATCGTTTTTGTTCCTGTGGACATCTAGTC 1440  
Qy 1441 ACTTGTAAACAATGTGTAAGCAGTGTGACAAGTGTCCCATGTGCTACACATCTACT 1500  
Db 1441 ACTTGTAAACAATGTGTAAGCAGTGTGACAAGTGTCCCATGTGCTACACATCTACT 1500  
Qy 1501 TTCAAGCAAAAATTTTATGCTTAATCTAACTCTATAGTAGGATGTTATGTTCT 1560  
Db 1501 TTCAAGCAAAAATTTTATGCTTAATCTAACTCTATAGTAGGATGTTATGTTCT 1560  
Qy 1561 TATTACCTGATTGAATGTGATGTGAATGACCTTTAAGTAATCAGGATGAAATCCAT 1620  
Db 1561 TATTACCTGATTGAATGTGATGTGAATGACCTTTAAGTAATCAGGATGAAATCCAT 1620  
Qy 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTTGGCAATATA 1680  
Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTGATTTTCAGGGTATTAGCTGTATATCCATTTTTTACTGTGA 1740  
Db 1681 ATCTTTGAATTTCTGATTTTCAGGGTATTAGCTGTATATCCATTTTTTACTGTGA 1740  
Qy 1741 TTTAATTGAACCATAGACTAAGAAATGAAGACATCACTAATCACTGAACAAATGTGT 1800  
Db 1741 TTTAATTGAACCATAGACTAAGAAATGAAGACATCACTAATCACTGAACAAATGTGT 1800  
Qy 1801 ATTATAGTAACTGATTTAATTTCTAAGTGAAGTAATTAATCATCTGGATTTTTAT 1860  
Db 1801 ATTATAGTAACTGATTTAATTTCTAAGTGAAGTAATTAATCATCTGGATTTTTAT 1860  
Qy 1861 TCTTTTCAGATAGGCTTAACAATGGAGCTTCTGTATATAATGTTGGAGATTAGATTA 1920  
Db 1861 TCTTTTCAGATAGGCTTAACAATGGAGCTTCTGTATATAATGTTGGAGATTAGATTA 1920  
Qy 1921 ATCTCCCCAATCACATAATTTGTTGTGTAAGGAAATAAATGTTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCCAATCACATAATTTGTTGTGTAAGGAAATAAATGTTTCCATGCTGGTG 1980  
Qy 1981 GAAAGATAGATTTGTTTATAGAGTTGGTTGTTGTTTATAGGATTTCTGTCCATTTCT 2040  
Db 1981 GAAAGATAGATTTGTTTATAGAGTTGGTTGTTGTTTATAGGATTTCTGTCCATTTCT 2040

Db 1981 GAAAGATAGATTTGTTTATAGAGTTGGTTGTTGTTTATAGGATTTCTGTCCATTTCT 2040  
Qy 2041 T 2041  
Db 2041 T 2041  
RESULT 7  
PCT-US02-11757-25  
; Sequence 25, Application PC/TUS0211757  
; GENERAL INFORMATION:  
; APPLICANT: PTC Therapeutics, Inc.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA  
; FILE REFERENCE: 10589-007-228  
; CURRENT APPLICATION NUMBER: PCT/US02/11757  
; CURRENT FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: 60/282,965  
; PRIOR FILING DATE: 2001-04-11  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 2540  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-11757-25  
Query Match 38.0%; Score 1990; DB 1; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GAAAAGGTGGCAAGTCCTATTTTCAAGAGAAAGATGACCTTTTAAACAGTTTGAAGGATCT 60  
Db 1 GAAAAGGTGGCAAGTCCTATTTTCAAGAGAAAGATGACCTTTTAAACAGTTTGAAGGATCT 60  
Qy 61 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAAATTTGTAGAAGTTTAATAGA 120  
Db 61 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAAATTTGTAGAAGTTTAATAGA 120  
Qy 121 TTAANAACCTTTTCTTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCAACACTGGCACGA 180  
Db 121 TTAANAACCTTTTCTTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCAACACTGGCACGA 180  
Qy 181 GCAGGTTTCTTTTATCTGTTGAAGGAGATACCGTGCCTGCTTTAGTTGTCTATGAGCT 240  
Db 181 GCAGGTTTCTTTTATCTGTTGAAGGAGATACCGTGCCTGCTTTAGTTGTCTATGAGCT 240  
Qy 241 GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAAGACACAGGAAAGTATCCCCAAAT 300  
Db 241 GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAAGACACAGGAAAGTATCCCCAAAT 300  
Qy 301 TGCAGATTTTATCAACGGCTTTTATCTTGAANAATAGTCCACGAGTCTACAAATTCGTGT 360  
Db 301 TGCAGATTTTATCAACGGCTTTTATCTTGAANAATAGTCCACGAGTCTACAAATTCGTGT 360  
Qy 361 ATCCAGAAATGGTCAGTACAAAGTTGAAAACATCTCGGGAAGCAGAGATCATTTTGCCTTA 420  
Db 361 ATCCAGAAATGGTCAGTACAAAGTTGAAAACATCTCGGGAAGCAGAGATCATTTTGCCTTA 420  
Qy 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAAGTGGGAGGTTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAAGTGGGAGGTTGTAGATATA 480  
Qy 481 TCAGACACCATATACCCGAGGAAACCTGCCATGTATAGTGAAGACCTAGATTAAGTCC 540  
Db 481 TCAGACACCATATACCCGAGGAAACCTGCCATGTATAGTGAAGACCTAGATTAAGTCC 540  
Qy 541 TTTTCAAGAACTGGCAGACTATGCTACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Db 541 TTTTCAAGAACTGGCAGACTATGCTACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Qy 601 TACTACACAGGTTTGGTGCACCAAGTGCAGTGTCTTTTGTGTTGGTGGAAAACCTGAAAAAT 660  
Db 601 TACTACACAGGTTTGGTGCACCAAGTGCAGTGTCTTTTGTGTTGGTGGAAAACCTGAAAAAT 660

Db 601 TACTACACAGGTATTTGGTGACCAAGTCAGTGTCTTTTGTGTGGTGAAGAACTGAAAAAT 660  
QY 661 TGGGAACCTTTGTGATCGTCTGCTGAGAACACAGAGGACACTTTCCTAAATTCGCTCTCTT 720  
Db 661 TGGGAACCTTTGTGATCGTCTGCTGAGAACACAGAGGACACTTTCCTAAATTCGCTCTCTT 720  
QY 721 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATCTGTGAGTCTGTGATAGGAAT 780  
Db 721 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATCTGTGAGTCTGTGATAGGAAT 780  
QY 781 TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATATGAAGCACGGATC 840  
Db 781 TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATATGAAGCACGGATC 840  
QY 841 TTTTACTTTTGGGACATGATATCTACTAGTTTAAAGTGAATCTGATCTGTGAGTCTGTGATAGGAAT 900  
Db 841 TTTTACTTTTGGGACATGATATCTACTAGTTTAAAGTGAATCTGATCTGTGAGTCTGTGATAGGAAT 900  
QY 901 TATGCTTTAGGTGAAGTGATATAAGTAAAGTGTCTTTTCACTGTGGAGGAGGCTTAACCTGAT 960  
Db 901 TATGCTTTAGGTGAAGTGATATAAGTAAAGTGTCTTTTCACTGTGGAGGAGGCTTAACCTGAT 960  
QY 961 TGGNAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAATAT 1020  
Db 961 TGGNAGCCCAAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAATAT 1020  
QY 1021 CTGTTAGAACAGAGGACAGAAATATATAACAATATTCATTTAACTCATTCACCTTGAG 1080  
Db 1021 CTGTTAGAACAGAGGACAGAAATATATAACAATATTCATTTAACTCATTCACCTTGAG 1080  
QY 1081 GAGTGTCTGTGAAGAACTACTGAGAAACACCACATCACTAACTAGAGAAATGATGATACC 1140  
Db 1081 GAGTGTCTGTGAAGAACTACTGAGAAACACCACATCACTAACTAGAGAAATGATGATACC 1140  
QY 1141 ATCTTCCAAATCCTATGGTACAGAGCTATACGATGGGTCAGTTTCAAGGACAT 1200  
Db 1141 ATCTTCCAAATCCTATGGTACAGAGCTATACGATGGGTCAGTTTCAAGGACAT 1200  
QY 1201 AAGAAATATGAGGAAAAATTCAGATATCTGGGAGCACTATAAATCACTTTGAGGTT 1260  
Db 1201 AAGAAATATGAGGAAAAATTCAGATATCTGGGAGCACTATAAATCACTTTGAGGTT 1260  
QY 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGTGAATGATCAAGTCAGACT 1320  
Db 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGTGAATGATCAAGTCAGACT 1320  
QY 1321 TCATTACAGAAACAGATTAGTACTGAGACAGCTAAGGCGCTGCAAGAGGAGAGCTT 1380  
Db 1321 TCATTACAGAAACAGATTAGTACTGAGACAGCTAAGGCGCTGCAAGAGGAGAGCTT 1380  
QY 1381 TGCAAAATCTGTATGGATAGAAATATTGCTATCTGTTTCTTCTGTTGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGTATGGATAGAAATATTGCTATCTGTTTCTTCTGTTGACATCTAGTC 1440  
QY 1441 ACTTGTAAACAATGCTGTGAAGCAGTTGACAAGTGTCCCATGTCTACACAGTCATTACT 1500  
Db 1441 ACTTGTAAACAATGCTGTGAAGCAGTTGACAAGTGTCCCATGTCTACACAGTCATTACT 1500  
QY 1501 TTCAAGCAAAAATTTTATGCTTAACTTAATCTATAGTAGGCATGTTATGTTCT 1560  
Db 1501 TTCAAGCAAAAATTTTATGCTTAACTTAATCTATAGTAGGCATGTTATGTTCT 1560  
QY 1561 TATTACCCCTGATTGGAATGTGTGATGTGAAGTGAATTTAAGTAATCAGGATTTGAATTTCCAT 1620  
Db 1561 TATTACCCCTGATTGGAATGTGTGATGTGAAGTGAATTTAAGTAATCAGGATTTGAATTTCCAT 1620  
QY 1621 TAGCATTGCTACCAAGTAGGAAAAAATGTATACATGGCAGTGTGTTAGTGTGCAATATA 1680  
Db 1621 TAGCATTGCTACCAAGTAGGAAAAAATGTATACATGGCAGTGTGTTAGTGTGCAATATA 1680  
QY 1681 ATCTTTGAAATTTCTGATTTTTCAGGATATAGCTGTATATCCATTTTTTACTGTTA 1740  
Db 1681 ATCTTTGAAATTTCTGATTTTTCAGGATATAGCTGTATATCCATTTTTTACTGTTA 1740

QY 1741 TTTAAATGAAACCATAGACTAAGAATAAAGACATCATACTATAACTGAACACAATGTGT 1800  
Db 1741 TTTAAATGAAACCATAGACTAAGAATAAAGACATCATACTATAACTGAACACAATGTGT 1800  
QY 1801 ATTCATAGTACTGATTTAAATTTCTTAAGTGAATTAATTAATCATCTCGATTTTTTAT 1860  
Db 1801 ATTCATAGTACTGATTTAAATTTCTTAAGTGAATTAATTAATCATCTCGATTTTTTAT 1860  
QY 1861 TCCTTTCAGATAGGCTTAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
Db 1861 TCCTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
QY 1921 ATCTCCCAATACATAAATTTGTTGTTGAAAAAGAAATAATTTCCATCTCGTGGTG 1980  
Db 1921 ATCTCCCAATACATAAATTTGTTGTTGAAAAAGAAATAATTTCCATCTCGTGGTG 1980  
QY 1981 GAAAGATAGAGATTGTTTTTAGAGGTTGGTTGTTGTTTTTAGGATTCTCTCCATTTTCT 2040  
Db 1981 GAAAGATAGAGATTGTTTTTAGAGGTTGGTTGTTGTTTTTAGGATTCTCTCCATTTTCT 2040  
QY 2041 T 2041  
Db 2041 T 2041

RESULT 8  
PCT-US02-11758-25  
; Sequence 25, Application PC/TUS0211758  
; GENERAL INFORMATION:  
; APPLICANT: PTC Therapeutics, Inc.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA  
; TITLE OF INVENTION: STRUCTURAL MOTIFS  
; FILE REFERENCE: 10589-008-228  
; CURRENT APPLICATION NUMBER: PCT/US02/11758  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 60/282,966  
; PRIOR FILING DATE: 2001-04-11  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 2540  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-11758-25

Query Match 38.0%; Score 1990; DB 1; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGTGGACAAGTCCTATTTTCAAGACAAGATGACTTTTAAACAGTTTGAAGGATCT 60  
Db 1 GAAAGGTGGACAAGTCCTATTTTCAAGACAAGATGACTTTTAAACAGTTTGAAGGATCT 60  
QY 61 AAAAATGTGTACTGTCAGACATCAATAAGGAAGAAGAAATTTGTAGAAGAGTTTAATAGA 120  
Db 61 AAAAATGTGTACTGTCAGACATCAATAAGGAAGAAGAAATTTGTAGAAGAGTTTAATAGA 120  
QY 121 TTAACAACTTTTCTTAATTTTCCAAAGTGTAGTCTGTTTCAGCATCAACACTGGCAGCA 180  
Db 121 TTAACAACTTTTCTTAATTTTCCAAAGTGTAGTCTGTTTCAGCATCAACACTGGCAGCA 180  
QY 181 GCAGGTTTCTTTTATCTGTTGAAGGAGATPACCGTGGGTCCTTTAGTCTCATGAGCT 240  
Db 181 GCAGGTTTCTTTTATCTGTTGAAGGAGATPACCGTGGGTCCTTTAGTCTCATGAGCT 240  
QY 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTTGGAGACACAGAAAGATATCCCAAAAT 300  
Db 241 GTAGATAGATGGCAATATGGAGACTCAGCAGTTTGGAGACACAGAAAGATATCCCAAAAT 300  
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTCCACGAGCTCTACAAATTTCTGGT 360  
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTCCACGAGCTCTACAAATTTCTGGT 360

Qy 361 ATCCAGAAATGCTCAGTACAAAGTTGAAAGTATCTGGGAAGCAGAGATCATTTTGCCTTA 420  
Db 361 ATCCAGAAATGCTCAGTACAAAGTTGAAAGTATCTGGGAAGCAGAGATCATTTTGCCTTA 420  
Qy 421 GACAGGCCATCTGAGACACATGCGAGACTATCTTTTGAGAACTGGCAGGTTGTAGATATA 480  
Db 421 GACAGGCCATCTGAGACACATGCGAGACTATCTTTTGAGAACTGGCAGGTTGTAGATATA 480  
Qy 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAGTCC 540  
Db 481 TCAGACACCATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAGTCC 540  
Qy 541 TTTGAGAACTGGCAGACTATGCTCAGCTAACCCCAAGAGAGTGTAGCAAGTCTGGAGTC 600  
Db 541 TTTGAGAACTGGCAGACTATGCTCAGCTAACCCCAAGAGAGTGTAGCAAGTCTGGAGTC 600  
Qy 601 TACTACACAGTATGCTGACCAAGTGCAGTGCCTTTTGTGGTGGAAACTGAAAT 660  
Db 601 TACTACACAGTATGCTGACCAAGTGCAGTGCCTTTTGTGGTGGAAACTGAAAT 660  
Qy 661 TGGGAACCTTGTGATCGTGCCTGCTGAGAACACAGGCGACACTTCCCTAAATTGCTTCCTT 720  
Db 661 TGGGAACCTTGTGATCGTGCCTGCTGAGAACACAGGCGACACTTCCCTAAATTGCTTCCTT 720  
Qy 721 GTTTTGGCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGAGTCTGTATAGGAAT 780  
Db 721 GTTTTGGCCGGAATCTTAATATTGGAAGTGAATCTGATGCTGAGTCTGTATAGGAAT 780  
Qy 781 TTCCCAATTCACAAATCTTCCCAAGAAATCCATCCATGGCAGATTAATGAAGCAGGATC 840  
Db 781 TTCCCAATTCACAAATCTTCCCAAGAAATCCATCCATGGCAGATTAATGAAGCAGGATC 840  
Qy 841 TTTACTTTTGGACATGATATACCTGCTTAAAGAGGAGCTTGAAGAGCTGGATTT 900  
Db 841 TTTACTTTTGGACATGATATACCTGCTTAAAGAGGAGCTTGAAGAGCTGGATTT 900  
Qy 901 TATGCTTTAGTGAAGTGAATAAGTAAAGTCTTCACTGTGGAGGAGGCTAACTGAT 960  
Db 901 TATGCTTTAGTGAAGTGAATAAGTAAAGTCTTCACTGTGGAGGAGGCTAACTGAT 960  
Qy 961 TGGAGCCCATGAGAGCCCTTGGGAACAACATGCTAAATGGTATCCAGGTCGCAATAT 1020  
Db 961 TGGAGCCCATGAGAGCCCTTGGGAACAACATGCTAAATGGTATCCAGGTCGCAATAT 1020  
Qy 1021 CTGTTAGAACAGAGGACAGAAATATATAACAATATTCATTTAACTCATTCCTTCAG 1080  
Db 1021 CTGTTAGAACAGAGGACAGAAATATATAACAATATTCATTTAACTCATTCCTTCAG 1080  
Qy 1081 GAGTGTCTGTAAGAACTTACTGAGAAACACCATCACTAAGAAATGATGATACC 1140  
Db 1081 GAGTGTCTGTAAGAACTTACTGAGAAACACCATCACTAAGAAATGATGATACC 1140  
Qy 1141 ATCTTCCAAAATCTATGTTACAGAAAGCTATAGAAATGGGGTTCAGTTTCAAGGACAT 1200  
Db 1141 ATCTTCCAAAATCTATGTTACAGAAAGCTATAGAAATGGGGTTCAGTTTCAAGGACAT 1200  
Qy 1201 AAGAAATAATGGAGGAAAAATTCAGATATCTGGGACCACTATAAATCACTTCAGGTT 1260  
Db 1201 AAGAAATAATGGAGGAAAAATTCAGATATCTGGGACCACTATAAATCACTTCAGGTT 1260  
Qy 1261 CTGGTTGAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320  
Db 1261 CTGGTTGAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320  
Qy 1321 TCATTACAGAAAGATAGTACTGAGAGAGCTATGAGGCGCTGCAAGAGAGAGGCTT 1380  
Db 1321 TCATTACAGAAAGATAGTACTGAGAGAGCTATGAGGCGCTGCAAGAGAGAGGCTT 1380  
Qy 1381 TGCAAAATCTGATGATAGAAATATGCTATCGTTTGTCTTGTGGACATCTAGTC 1440  
Db 1381 TGCAAAATCTGATGATAGAAATATGCTATCGTTTGTCTTGTGGACATCTAGTC 1440

Qy 1441 ACTTGTAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCAATTA 1500  
Db 1441 ACTTGTAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCAATTA 1500  
Qy 1501 TTCAGCAAAAATTTTATGCTTAATCTAACTAACTATAGTAGGCACTGTATGTTGTTCT 1560  
Db 1501 TTCAGCAAAAATTTTATGCTTAATCTAACTAACTATAGTAGGCACTGTATGTTGTTCT 1560  
Qy 1561 TATTACCCCTGATGATGTAAGTGAACCTGACCTTTAAGTAATCAGGATTTGAAATCCAT 1620  
Db 1561 TATTACCCCTGATGATGTAAGTGAACCTGACCTTTAAGTAATCAGGATTTGAAATCCAT 1620  
Qy 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTGGCAATATA 1680  
Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTGTTAGTGGCAATATA 1680  
Qy 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTACTGTTA 1740  
Db 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTACTGTTA 1740  
Qy 1741 TTTAATTGAAACCATAGACTAAGATAAAGAGCATCATATAACTGAACAATGTT 1800  
Db 1741 TTTAATTGAAACCATAGACTAAGATAAAGAGCATCATATAACTGAACAATGTT 1800  
Qy 1801 ATTCATAGTATGATTAATTTCTAAAGTGAAGTGAATTAATCATCTGGATTTTAT 1860  
Db 1801 ATTCATAGTATGATTAATTTCTAAAGTGAAGTGAATTAATCATCTGGATTTTAT 1860  
Qy 1861 TCTTTTCAGATAGGCTTAACAAATGAGCTTCTCTATATATAATGTGGAGATTAGTTA 1920  
Db 1861 TCTTTTCAGATAGGCTTAACAAATGAGCTTCTCTATATATAATGTGGAGATTAGTTA 1920  
Qy 1921 ATCTCCCCAATCACATAATTTGTTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980  
Db 1921 ATCTCCCCAATCACATAATTTGTTGTGAAAAAGGAATAAATGTTCCATGCTGGTG 1980  
Qy 1981 GAAAGATAGAGATGTTTTTAGAGGTTGTTGTTGTTTGTAGGATTCGTCCATTTTCT 2040  
Db 1981 GAAAGATAGAGATGTTTTTAGAGGTTGTTGTTGTTTGTAGGATTCGTCCATTTTCT 2040  
Qy 2041 T 2041  
Db 2041 T 2041

## RESULT 9

US-08-576-956-3

; Sequence 3, Application US/08576956

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G.

; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Baird, Stephen

; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/576,956

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/511,485

; FILING DATE: 04-AUG-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 07891/002001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2540 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: DNA (genomic)  
US-08-576-956-3

Query Match 38.0%; Score 1990; DB 9; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GAAAGGTGACAGTCTATTTTCAAGACAGATGACTTTTAAACAGTCTTTGAAGGATCT	60
DB	1	GAAAGGTGACAGTCTATTTTCAAGACAGATGACTTTTAAACAGTCTTTGAAGGATCT	60
QY	61	AAAACCTTTGCTACTGTCAGACATCAATAAGGAAGAAGATTTGTAGAAGAGTTTAATAGA	120
DB	61	AAAACCTTTGCTACTGTCAGACATCAATAAGGAAGAAGATTTGTAGAAGAGTTTAATAGA	120
QY	121	TTAAAACTTTTGTCTAATTTTCCAAAGTGTAGTCTCTTTTCAACATCAACACATGGCACA	180
DB	121	TTAAAACTTTTGTCTAATTTTCCAAAGTGTAGTCTCTTTTCAACATCAACACATGGCACA	180
QY	181	GCAGGTTTCTTATCTGTCGAGAGATACCGTGGCGTCTTTAGTTGTCATGAGCT	240
DB	181	GCAGGTTTCTTATCTGTCGAGAGATACCGTGGCGTCTTTAGTTGTCATGAGCT	240
QY	241	GTAGATAGTGGCAATATGAGACTCAGCAGTGTGGGAAGACACAGGAAGTATCCCAAAAT	300
DB	241	GTAGATAGTGGCAATATGAGACTCAGCAGTGTGGGAAGACACAGGAAGTATCCCAAAAT	300
QY	301	TGCAGATTTATCAACGGCTTTTATCTGTGAAATAGTGTCCACGAGTCTACAAAATCTGGT	360
DB	301	TGCAGATTTATCAACGGCTTTTATCTGTGAAATAGTGTCCACGAGTCTACAAAATCTGGT	360
QY	361	ATCCAGATGGTCAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCAATTTGGCTTA	420
DB	361	ATCCAGATGGTCAGTACAAAGTTGAAACTATCTGGGAAGCAGAGATCAATTTGGCTTA	420
QY	421	GACAGGCTCTCTGAGACACATGACAGTCTATCTTTTGGAACTGGCAGGTTGTAGATATA	480
DB	421	GACAGGCTCTCTGAGACACATGACAGTCTATCTTTTGGAACTGGCAGGTTGTAGATATA	480
QY	481	TCAGACACCATATACCCGAGAACCCCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC	540
DB	481	TCAGACACCATATACCCGAGAACCCCTGCCATGTATGTGAAGAAGCTAGATTAAAGTCC	540
QY	541	TTTCAGAACTGGCCAGACTATGCTACCTTAACCCCAAGAGAGTTAGCAAGTGTGGACTC	600
DB	541	TTTCAGAACTGGCCAGACTATGCTACCTTAACCCCAAGAGAGTTAGCAAGTGTGGACTC	600
QY	601	TACTACACAGTATTGGTGACCAAGTGCAGTGTCTTTGTTGGTGGAAACCTGAAAAAT	660
DB	601	TACTACACAGTATTGGTGACCAAGTGCAGTGTCTTTGTTGGTGGAAACCTGAAAAAT	660
QY	661	TGGGAACCTTTGTATGCTGCTGGTTCAGAACACAGCGCAGACATTTCTCTAATTCCTTTT	720
DB	661	TGGGAACCTTTGTATGCTGCTGGTTCAGAACACAGCGCAGACATTTCTCTAATTCCTTTT	720
QY	721	GTGTTGGCGGGAATCTTAATATTCGAAGTGAATCTGAGTCTGATGAGGAAT	780
DB	721	GTGTTGGCGGGAATCTTAATATTCGAAGTGAATCTGAGTCTGATGAGGAAT	780

DB	721	GTGTTGGCGGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT	780
QY	781	TTCCCAAAATTCACAAATCTTTCCAAAGAAATCCATCCATGGCAGATTTATGAAGCAGCATC	840
DB	781	TTCCCAAAATTCACAAATCTTTCCAAAGAAATCCATCCATGGCAGATTTATGAAGCAGCATC	840
QY	841	TTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGGAGCAGCTTGCACAGAGCTGGATTT	900
DB	841	TTTACTTTTGGGACATGGATATATCTCAGTTTAAACAAGGAGCAGCTTGCACAGAGCTGGATTT	900
QY	901	TATGCTTTAGTGTGAAGTGAATAAGTGTCTTTTCTGAGGAGGCTAACTGAT	960
DB	901	TATGCTTTAGTGTGAAGTGAATAAGTGTCTTTTCTGAGGAGGCTAACTGAT	960
QY	961	TGGAAGCCCAAGTGAAGACCTTGGGAACAACATCTAAATGGTATCCAGGCTGCAATAT	1020
DB	961	TGGAAGCCCAAGTGAAGACCTTGGGAACAACATCTAAATGGTATCCAGGCTGCAATAT	1020
QY	1021	CTGTTAGACAGAGGAGGACAAAGATATATAAACAATATTCATTTAACTCATTTGAG	1080
DB	1021	CTGTTAGACAGAGGAGGACAAAGATATATAAACAATATTCATTTAACTCATTTGAG	1080
QY	1081	GAGTGTCTGTAGAACTACTGAGAAAACACCATCACTAACTAGAGAATTTGATATACC	1140
DB	1081	GAGTGTCTGTAGAACTACTGAGAAAACACCATCACTAACTAGAGAATTTGATATACC	1140
QY	1141	ATCTTCCAAAATCCTATGTTACAAAGAGCTATACGAATGGGTTTCAAGGACATTT	1200
DB	1141	ATCTTCCAAAATCCTATGTTACAAAGAGCTATACGAATGGGTTTCAAGGACATTT	1200
QY	1201	AAGAAAATTAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGTT	1260
DB	1201	AAGAAAATTAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTTGAGTT	1260
QY	1261	CTGGTTCACATCTAGTGAATGCTCAGAAAGACAGATGCAAGATGAGTCAAGTCAAGT	1320
DB	1261	CTGGTTCACATCTAGTGAATGCTCAGAAAGACAGATGCAAGATGAGTCAAGTCAAGT	1320
QY	1321	TCATTCAGAAAAGAGATTAGTACTGAAAGCAGCTTAAGGCCCTGCAAGAGGAGAGCTT	1380
DB	1321	TCATTCAGAAAAGAGATTAGTACTGAAAGCAGCTTAAGGCCCTGCAAGAGGAGAGCTT	1380
QY	1381	TGCAAAATCTGTATGGATAGAAAATTTGCTATCTGTTTTTCTGTTGACATCTAGT	1440
DB	1381	TGCAAAATCTGTATGGATAGAAAATTTGCTATCTGTTTTTCTGTTGACATCTAGT	1440
QY	1441	ACTTGTAAACAATGCTGTCGAGCAGTTGCAAGTGTCCCATGCTCACAGTCAATTACT	1500
DB	1441	ACTTGTAAACAATGCTGTCGAGCAGTTGCAAGTGTCCCATGCTCACAGTCAATTACT	1500
QY	1501	TTCAAGCAAAAATTTTATGCTTAACTCTATAGTAGGATGTTATGTTGTTCT	1560
DB	1501	TTCAAGCAAAAATTTTATGCTTAACTCTATAGTAGGATGTTATGTTGTTCT	1560
QY	1561	TATTACCTGATTGAATGTGTGATGTGAAGTCTTAACTTAATTCAGGATTTGAATTCAT	1620
DB	1561	TATTACCTGATTGAATGTGTGATGTGAAGTCTTAACTTAATTCAGGATTTGAATTCAT	1620
QY	1621	TAGCATTTGCTACAGTAGGAAAAAATGTCATGCGGAGTGTGTTAGTTGGCAATATA	1680
DB	1621	TAGCATTTGCTACAGTAGGAAAAAATGTCATGCGGAGTGTGTTAGTTGGCAATATA	1680
QY	1681	ATCTTTGAATTTCTGATTTTTCAGGTTTACTGTTATTCATTTTCTTACTGTTA	1740
DB	1681	ATCTTTGAATTTCTGATTTTTCAGGTTTACTGTTATTCATTTTCTTACTGTTA	1740
QY	1741	TTTAAATGAACCATAGACTTAAGAATAAGAACATCATATAACTTGAACAAATGTGT	1800
DB	1741	TTTAAATGAACCATAGACTTAAGAATAAGAACATCATATAACTTGAACAAATGTGT	1800
QY	1801	ATTTCATAGTATCTGATTTAATTTTCAAGTGAATTAATCATCTCGATTTTAT	1860
DB	1801	ATTTCATAGTATCTGATTTAATTTTCAAGTGAATTAATCATCTCGATTTTAT	1860

Qy	1861	TCTTTTCAGATAGGCTTAACAATGGAGCTTTCGTATATAAAATGTGGAGATTAGACTTA	1920
Db	1861	TCTTTTCAGATAGGCTTAACAATGGAGCTTTCGTATATAAAATGTGGAGATTAGACTTA	1920
Qy	1921	ATCTCCCCAATCACATAATTTGTTTTGTGTGAANAAGGAATAAATTTGTTCCATGCTGGTG	1980
Db	1921	ATCTCCCCAATCACATAATTTGTTTTGTGTGAANAAGGAATAAATTTGTTCCATGCTGGTG	1980
Qy	1981	GAAAGATAGAGATTGTTTTTAGAGGTGGTGTCTGTTTGTAGGATTCTGTGCCAATTTTCT	2040
Db	1981	GAAAGATAGAGATTGTTTTTAGAGGTGGTGTCTGTTTGTAGGATTCTGTGCCAATTTTCT	2040
Qy	2041	T 2041	
		-	
Db	2041	T 2041	

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RESULT 10
US-08-576-956A-3
; Sequence 3, Application US/08576956A
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq Version 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/576,956A
; FILING DATE: 22-DEC-95
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/511,485
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07891/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; . SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-576-956A-3

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Qy	61	AAAACTGTGTACCTGCAGACATCAATTAAGGAAGAAATTTGTAGAAAGAGTTTAATAGA	120
Db	61	AAAACTGTGTACCTGCAGACATCAATTAAGGAAGAAATTTGTAGAAAGAGTTTAATAGA	120
Qy	121	TTAAAACTTTTGCCTAAATTTTCCAAAGTGGTAGTCTGCTTTTCAGCATCAACACATGGCAGCA	180
Db	121	TTAAAACTTTTGCCTAAATTTTCCAAAGTGGTAGTCTGCTTTTCAGCATCAACACATGGCAGCA	180
Qy	181	GCAGGGTTCTTTATCTACTGGTGAAGGAGATACCGTGCGGTGCTTTAGTTGTCTATCGAGCT	240
Db	181	GCAGGGTTCTTTATCTACTGGTGAAGGAGATACCGTGCGGTGCTTTAGTTGTCTATCGAGCT	240
Qy	241	GTAGATAGATGGCAATATATGGAGACTTCAGAGTGTGGAAGACACAGAAAGATATCCCAAAT	300
Db	241	GTAGATAGATGGCAATATATGGAGACTTCAGAGTGTGGAAGACACAGAAAGATATCCCAAAT	300
Qy	301	TGCAGATTTATCAAGGGCTTTTATCTCTGAAATAGTCCAGCGAGTCTACAAATTTCTGGT	360
Db	301	TGCAGATTTATCAAGGGCTTTTATCTCTGAAATAGTCCAGCGAGTCTACAAATTTCTGGT	360
Qy	361	ATCCAGAAATGGTCAAGTGTACAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGCTTTA	420
Db	361	ATCCAGAAATGGTCAAGTGTACAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGCTTTA	420
Qy	421	GACAGGCCATCTGAGACACATCGAGACTATCTTTTGAAGACTGGCGAGTGTGATGATATA	480
Db	421	GACAGGCCATCTGAGACACATCGAGACTATCTTTTGAAGACTGGCGAGTGTGATGATATA	480
Qy	481	TCAGACACCATATATCCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAAGTCC	540
Db	481	TCAGACACCATATATCCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAAGTCC	540
Qy	541	TTTCAGAACTGGCCAGACTATGCTCACCTTAACCCCAAGAGAGTTAGCAAGTGTGTGAGCT	600
Db	541	TTTCAGAACTGGCCAGACTATGCTCACCTTAACCCCAAGAGAGTTAGCAAGTGTGTGAGCT	600
Qy	601	TACTACACAGGTATTTGGTGACCAAGTGCAGTGCTTTTGTGTGTGGAAGTGAAGAAAT	660
Db	601	TACTACACAGGTATTTGGTGACCAAGTGCAGTGCTTTTGTGTGTGGAAGTGAAGAAAT	660
Qy	661	TGGGAACCTTGTGATCGTGCCTGGTTCAGAACACAGCGGACACTTTCCTAATTGCTTCTTTT	720
Db	661	TGGGAACCTTGTGATCGTGCCTGGTTCAGAACACAGCGGACACTTTCCTAATTGCTTCTTTT	720
Qy	721	GTTTTGGGCCGGAACTTTAATATTCCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT	780
Db	721	GTTTTGGGCCGGAACTTTAATATTCCGAAGTGAATCTGATGCTGTGAGTCTCTGATAGGAAT	780
Qy	781	TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATATATGAAGCACGGATC	840
Db	781	TTCCCAAAATTCACAAATCTTCCAGAAATCCATCCATGGCAGATATATGAAGCACGGATC	840
Qy	841	TTTACTTTTGGGCATGGATATACTACAGTAAACAGGAGCAGCTTTCGAAAGCTGGATTT	900
Db	841	TTTACTTTTGGGCATGGATATACTACAGTAAACAGGAGCAGCTTTCGAAAGCTGGATTT	900
Qy	901	TATGCTTTAGGTGAAGGTGATATAAGTAAAGTCTTTCCTACTCTGAGGAGGGCTAACTGAT	960
Db	901	TATGCTTTAGGTGAAGGTGATATAAGTAAAGTCTTTCCTACTCTGAGGAGGGCTAACTGAT	960
Qy	961	TGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAAT	1020
Db	961	TGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAAT	1020
Qy	1021	CTGTTTGAACAGAGGGACAGAAATATATAACAATATTTCAATTAACTCATTTCACTTGAG	1080
Db	1021	CTGTTTGAACAGAGGGACAGAAATATATAACAATATTTCAATTAACTCATTTCACTTGAG	1080
Qy	1081	GAGTGTCTGTAGAACTACTCAGAAAAACACCATCACTACAACTAGAGAAATTGATGATACC	1140
Db	1081	GAGTGTCTGTAGAACTACTCAGAAAAACACCATCACTACAACTAGAGAAATTGATGATACC	1140
Qy	1141	ATCTTCCAAAATCCTATGTGTACAAGAAGCTATACGAATTGGGGTTTCAGTTTCAAGGACATT	1200

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Db 1141 ATCTTCAAAATCCTATGGTACAAAGAGCTATACGAATGGGTTCAGTTTCARAGGACATT 1200
QY 1201 AAGAAATATAGGAGAAAAATTCAGATATCTGGGAGCAACTATAAATCAGTTGAGGTT 1260
Db 1201 AAGAAATATAGGAGAAAAATTCAGATATCTGGGAGCAACTATAAATCAGTTGAGGTT 1260
QY 1261 CTGGTGCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320
Db 1261 CTGGTGCAGATCTAGTGAATGCTCAGAAAGACAGATATGCAAGATGAGTCAAGTCAGACT 1320
QY 1321 TCATTACAGAAAGAGATAGTACTGAGAGCAGCTTAAGCGCCTGCAAGAGGAGAGCTT 1380
Db 1321 TCATTACAGAAAGAGATAGTACTGAGAGCAGCTTAAGCGCCTGCAAGAGGAGAGCTT 1380
QY 1381 TGCAAAATCTGTATGGATAGAAAATATGCTTATCGTTTTCCTTGTGGACATCTAGTC 1440
Db 1381 TGCAAAATCTGTATGGATAGAAAATATGCTTATCGTTTTCCTTGTGGACATCTAGTC 1440
QY 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT 1500
Db 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT 1500
QY 1501 TTCACGCAAAAATTTTATGCTTAACTCTAAGAGCAGTATAGTAGGCATGTTATGTTCT 1560
Db 1501 TTCACGCAAAAATTTTATGCTTAACTCTAAGAGCAGTATAGTAGGCATGTTATGTTCT 1560
QY 1561 TATTACCTGATTGAATGTGTGATGTGAAGTGAATTAAGTAATCAGGATTAATTCCTAT 1620
Db 1561 TATTACCTGATTGAATGTGTGATGTGAAGTGAATTAAGTAATCAGGATTAATTCCTAT 1620
QY 1621 TAGCATTGCTACCAAGTAGGAAAAAATGTACATGGCAGTCTTTTAGTTGGCAATATA 1680
Db 1621 TAGCATTGCTACCAAGTAGGAAAAAATGTACATGGCAGTCTTTTAGTTGGCAATATA 1680
QY 1681 ATCTTTGAATTTCTGATTTTCAGGGTATAGCTGTATATCCATTTTTTACTGTTA 1740
Db 1681 ATCTTTGAATTTCTGATTTTCAGGGTATAGCTGTATATCCATTTTTTACTGTTA 1740
QY 1741 TTTTAATGAAACCATAGACTAAGAATAAAGAGCATCATACTATACTGAACACAATGTGT 1800
Db 1741 TTTTAATGAAACCATAGACTAAGAATAAAGAGCATCATACTATACTGAACACAATGTGT 1800
QY 1801 ATTCATAGTACTGATTTAATTTCTAAGTGTAAAGTCAATTAATCATCTGGATTTTTAT 1860
Db 1801 ATTCATAGTACTGATTTAATTTCTAAGTGTAAAGTCAATTAATCATCTGGATTTTTAT 1860
QY 1861 TCCTTTTCAGATAGGCTTAACAATGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
Db 1861 TCCTTTTCAGATAGGCTTAACAATGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
QY 1921 ATCTCCCAATCACAATAATTTGTTGTGTAAGAAAGGAATAAATGTTCCATGCTGGTG 1980
Db 1921 ATCTCCCAATCACAATAATTTGTTGTGTAAGAAAGGAATAAATGTTCCATGCTGGTG 1980
QY 1981 GAAAGATAGAGATGTTTTAGAGTTGGTGTGTTGTTTTAGGATTCGTCCATTTTCT 2040
Db 1981 GAAAGATAGAGATGTTTTAGAGTTGGTGTGTTGTTTTAGGATTCGTCCATTTTCT 2040
QY 2041 T 2041
Db 2041 T 2041
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RESULT 11
US-09-011-356-3
; Sequence 3, Application US/09011356
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
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; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT APPLICATION NUMBER: US/09/011,356
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-011-356-3
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Query Match 38.0%; Score 1990; DB 14; Length 2540;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GAAAGGTGGACAAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTTGAAGGATCT 60
Db 1 GAAAGGTGGACAAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTTGAAGGATCT 60
QY 61 AAAACCTTGTTGTAACCTGCAGACATCAATAAGGAAGAAGAATTTGTAGAAGAGTTTAATAGA 120
Db 61 AAAACCTTGTTGTAACCTGCAGACATCAATAAGGAAGAAGAATTTGTAGAAGAGTTTAATAGA 120
QY 121 TTAATAACCTTTTCTTAATTTTCCAAGTGGTAGTCCTGTTTTCAGCATCAACACTGGCAGCA 180
Db 121 TTAATAACCTTTTCTTAATTTTCCAAGTGGTAGTCCTGTTTTCAGCATCAACACTGGCAGCA 180
QY 181 GCAGGTTTCTTTATACTGTTGAAGGAGATACCGTGGGTGCTTTAGTTTGTCTCATGCGAGCT 240
Db 181 GCAGGTTTCTTTATACTGTTGAAGGAGATACCGTGGGTGCTTTAGTTTGTCTCATGCGAGCT 240
QY 241 GTAGATAGATGGCAATATATGGAGACTCAGCAGTTGGGAAGACACAGGAAGATATCCCCAAAT 300
Db 241 GTAGATAGATGGCAATATATGGAGACTCAGCAGTTGGGAAGACACAGGAAGATATCCCCAAAT 300
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAAGTAGTCCACGCGAGTCTACAAATTTCTGGT 360
Db 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAAGTAGTCCACGCGAGTCTACAAATTTCTGGT 360
QY 361 ATCCAGAATGGTCAGTACAAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGGCTTA 420
Db 361 ATCCAGAATGGTCAGTACAAAAGTTGAAAACATCTCTGGGAAGCAGAGATCATTTTGGCTTA 420
QY 421 GACAGGCCATCTCAGACACATATGCAAGTATCTTTTGTAGAAGTGGCAGGTTGTAGATATA 480
Db 421 GACAGGCCATCTCAGACACATATGCAAGTATCTTTTGTAGAAGTGGCAGGTTGTAGATATA 480
QY 481 TCAGACACCATATATACCGGAGAACCTGCCATCTATAGTCAACAAGCTAGATTAAGTCC 540
Db 481 TCAGACACCATATATACCGGAGAACCTGCCATCTATAGTCAACAAGCTAGATTAAGTCC 540
QY 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600
Db 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600
QY 601 TACTACACAGGTTATGGTGACCAAGTGCAGTGTCTTTTGTGGTGGTGAACCTGAAAAAT 660
Db 601 TACTACACAGGTTATGGTGACCAAGTGCAGTGTCTTTTGTGGTGGTGAACCTGAAAAAT 660
QY 661 TGGGAACCTTGTGATCGTCTGTCAGAACACAGCGGACACTTTCTTAATTCCTCTTT 720
Db 661 TGGGAACCTTGTGATCGTCTGTCAGAACACAGCGGACACTTTCTTAATTCCTCTTT 720
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QY 721 GTTTGGCCGGAATCTTAATATTCGAAGTAATCTGATGCTGAGTCTCTGATAGGAAT 780
DB 721 GTTTGGCCGGAATCTTAATATTCGAAGTAATCTGATGCTGAGTCTCTGATAGGAAT 780
QY 781 TTCCCAAAATCAACAAATCTTCCCAAGAAATCCATCCATGGCAGATATTAAGACGCGATC 840
DB 781 TTCCCAAAATCAACAAATCTTCCCAAGAAATCCATCCATGGCAGATATTAAGACGCGATC 840
QY 841 TTTACTTTTGGACATGATATACCTACCTTACCAAGGAGCAGCTTGCAGAGCTGGATTT 900
DB 841 TTTACTTTTGGACATGATATACCTACCTTACCAAGGAGCAGCTTGCAGAGCTGGATTT 900
QY 901 TATGCTTTTGGTGAAGGTGATAAGCTAAAGTCTTCTACTGTGGAGGAGGGCTAACTGAT 960
DB 901 TATGCTTTTGGTGAAGGTGATAAGCTAAAGTCTTCTACTGTGGAGGAGGGCTAACTGAT 960
QY 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATAT 1020
DB 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAAATAT 1020
QY 1021 CTGTTAGAACAGAGGACAGAATATATAACATAATTCATTTAACTCACTTCCTTGAG 1080
DB 1021 CTGTTAGAACAGAGGACAGAATATATAACATAATTCATTTAACTCACTTCCTTGAG 1080
QY 1081 GAGTGTCTGGTAAGAACTACTGAGAAAAACACCATCACTAACTAGAGAATTCATGATACC 1140
DB 1081 GAGTGTCTGGTAAGAACTACTGAGAAAAACACCATCACTAACTAGAGAATTCATGATACC 1140
QY 1141 ATCTTCCAAAATCCCTATGGTACAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACAT 1200
DB 1141 ATCTTCCAAAATCCCTATGGTACAAGAGCTATACGAATGGGGTTCAGTTTCAAGGACAT 1200
QY 1201 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCACTATAAATCACTTCAGGTT 1260
DB 1201 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCACTATAAATCACTTCAGGTT 1260
QY 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACATATGCAAGATGAGTCAAGTCAGACT 1320
DB 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACATATGCAAGATGAGTCAAGTCAGACT 1320
QY 1321 TCATTACAGAAAGAGATTAGTACTCAAGAGCAGCTAAGCGCCCTCAAGAGGAGAGCTT 1380
DB 1321 TCATTACAGAAAGAGATTAGTACTCAAGAGCAGCTAAGCGCCCTCAAGAGGAGAGCTT 1380
QY 1381 TCCAAATCTGTATGGATAGAAATATGCTATCGTTTTTGTCCCTTGGACATCTAGTC 1440
DB 1381 TCCAAATCTGTATGGATAGAAATATGCTATCGTTTTTGTCCCTTGGACATCTAGTC 1440
QY 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGCTCATCT 1500
DB 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGCTCATCT 1500
QY 1501 TTCAGCAAAAATTTTATGCTTAACTAATCTATAGTAGGAGATGTATGTTGTTCT 1560
DB 1501 TTCAGCAAAAATTTTATGCTTAACTAATCTATAGTAGGAGATGTATGTTGTTCT 1560
QY 1561 TATTACCTGATTGATGTGATGTGAATGACCTTTTAACTTAACTCAGGATTCATTCAT 1620
DB 1561 TATTACCTGATTGATGTGATGTGAATGACCTTTTAACTTAACTCAGGATTCATTCAT 1620
QY 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGPACATGGCAGTGTTTTAGTTGGCAATATA 1680
DB 1621 TAGCAATTTGCTACCAAGTAGGAAAAAATGPACATGGCAGTGTTTTAGTTGGCAATATA 1680
QY 1681 ATCTTTGAATTTCTTGAATTTTTCAGGGTATAGCTGTATATPCCATTTTTTACTGTGTA 1740
DB 1681 ATCTTTGAATTTCTTGAATTTTTCAGGGTATAGCTGTATATPCCATTTTTTACTGTGTA 1740
QY 1741 TTTAATTTGAACCATAGACTAAGAAATAGAGCATCATCTAATTAATTAATTAATTAATTAAT 1800
DB 1741 TTTAATTTGAACCATAGACTAAGAAATAGAGCATCATCTAATTAATTAATTAATTAATTAAT 1800
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QY 1801 ATTCTAGTACTGATTAATTTCTAAGTGTAAAGTAATTAATCATCTGGATTTTTTAT 1860
DB 1801 ATTCTAGTACTGATTAATTTCTAAGTGTAAAGTAATTAATCATCTGGATTTTTTAT 1860
QY 1861 TCTTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAAGATTA 1920
DB 1861 TCTTTTCAGATAGGCTTAAACAAATGGAGCTTCTGTATATAAATGTGGAGATTAAGATTA 1920
QY 1921 ATCTCCCAATCACATAATTTCTGTTGTAAGAAAGGAATAAATGTTCCATGCTGGTG 1980
DB 1921 ATCTCCCAATCACATAATTTCTGTTGTAAGAAAGGAATAAATGTTCCATGCTGGTG 1980
QY 1981 GAAAGATAGAGATTTTCTAGAGTGTGTTGTTTGTAGGATTCGTCCATTTCT 2040
DB 1981 GAAAGATAGAGATTTTCTAGAGTGTGTTGTTTGTAGGATTCGTCCATTTCT 2040
QY 2041 T 2041
DB 2041 T 2041

RESULT 12
US-09-011-356-3
; Sequence 3, Application US/09011356A
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003002
; CURRENT FILLING DATE: US/09/011, 356A
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILLING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILLING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILLING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-011-356-3

Query Match 38.0%; Score 1990; DB 14; Length 2540;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAAGGTGGAACAAGTCCCTATTTCGAAGAGAGAGATGACCTTTTAAACAGTTTGAAGATCT 60
DB 1 GAAAAGGTGGAACAAGTCCCTATTTCGAAGAGAGAGATGACCTTTTAAACAGTTTGAAGATCT 60
QY 61 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAGAAATTTGTAGAAGATTTAATAGA 120
DB 61 AAAACTGTGTACCTGCAGACATCAATAAGGAAGAGAAATTTGTAGAAGATTTAATAGA 120
QY 121 TTAATAACTTTTGTCTAATTTTCCAGTGGTAGTCTGTTTCCAGCATCAACACTGGCACGA 180
DB 121 TTAATAACTTTTGTCTAATTTTCCAGTGGTAGTCTGTTTCCAGCATCAACACTGGCACGA 180
QY 181 GCAGGGTTTCTTTATCTACTGGTGAAGGAGATACCGTCGGTGTCTTTAGTTGTCTATGAGCT 240
DB 181 GCAGGGTTTCTTTATCTACTGGTGAAGGAGATACCGTCGGTGTCTTTAGTTGTCTATGAGCT 240
QY 241 GTAGATAGATGCAANTATGGAGACTCAGCAGTTTGGAAAGACACAGGAAAGTATCCCCCAAT 300
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023.655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 900:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2540 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g1184319  
; US-09-023-655-900

Query Match 38.0%; Score 1990; DB 14; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GAAAAGTGGCAAGTCTCTATTTCAGAGAGAGATGACTTTTAACAGTCTTTGAAGGATCT 60  
DB 1 GAAAAGTGGCAAGTCTCTATTTCAGAGAGAGATGACTTTTAACAGTCTTTGAAGGATCT 60  
  
QY 61 AAACTTGTGTACCTGCGACACATCAATTAAGGAAGAAATTTGTAGAGAGTTTAATAGA 120  
DB 61 AAACTTGTGTACCTGCGACACATCAATTAAGGAAGAAATTTGTAGAGAGTTTAATAGA 120  
  
QY 121 TTAATAACTTTTGTCTAAATTTTCCAAAGTGTGTCTCTGTTTACAGCATCAACACTGGCACA 180  
DB 121 TTAATAACTTTTGTCTAAATTTTCCAAAGTGTGTCTCTGTTTACAGCATCAACACTGGCACA 180  
  
QY 181 GCAGGGTTCTTTTACTGGTGAAGAGATACCGTGCCTGCTTTAGTTGTCTATGCAGCT 240  
DB 181 GCAGGGTTCTTTTACTGGTGAAGAGATACCGTGCCTGCTTTAGTTGTCTATGCAGCT 240  
  
QY 241 GTAGATAGATGCCAATATGGAGACTCAGCAGTTGGAGACACAGGAAGATATCCCAAT 300  
DB 241 GTAGATAGATGCCAATATGGAGACTCAGCAGTTGGAGACACAGGAAGATATCCCAAT 300  
  
QY 301 TGCAGATTATCAACGGCTTTTATCTTGAATAAGTAGTCCACGCTCTACAAATTTCTGGT 360  
DB 301 TGCAGATTATCAACGGCTTTTATCTTGAATAAGTAGTCCACGCTCTACAAATTTCTGGT 360  
  
QY 361 ATCCAGATGGTCACTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA 420  
DB 361 ATCCAGATGGTCACTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA 420  
  
QY 421 GACAGGCCATCTGACACATGACAGACTATCTTTTGAAGTGGCAGGTTGTAGATATA 480  
DB 421 GACAGGCCATCTGACACATGACAGACTATCTTTTGAAGTGGCAGGTTGTAGATATA 480  
  
QY 481 TCAGACACATATACCGAGGAACCCCTGCCATGTATAGTGAAGAGCTAGATTAAGTCC 540  
DB 481 TCAGACACATATACCGAGGAACCCCTGCCATGTATAGTGAAGAGCTAGATTAAGTCC 540  
  
QY 541 TTTTCAAGTGGCAGACTATGCTCACCTTAACCCCAAGAGAGTTAGCAGTCTGGACTC 600  
DB 541 TTTTCAAGTGGCAGACTATGCTCACCTTAACCCCAAGAGAGTTAGCAGTCTGGACTC 600  
  
QY 601 TACTACAGGTTATGGTGACCAAGTGCAGTCTTTTGTGGTGGAAACTGAAAT 660  
DB 601 TACTACAGGTTATGGTGACCAAGTGCAGTCTTTTGTGGTGGAAACTGAAAT 660

QY 661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTTCCTAAATGCTTCTTT 720  
DB 661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGCGACACTTTCCTAAATGCTTCTTT 720  
  
QY 721 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT 780  
DB 721 GTTTTGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT 780  
  
QY 781 TTCCCAAAATTCACAAATCTTCCAAAGATCCATCCATGGCAGATATGAAGCAGGATC 840  
DB 781 TTCCCAAAATTCACAAATCTTCCAAAGATCCATCCATGGCAGATATGAAGCAGGATC 840  
  
QY 841 TTTACTTTTGGACATGGATATACACTCAGTTAAACAGGAGCAGCTTGAAGAGCTGGATTT 900  
DB 841 TTTACTTTTGGACATGGATATACACTCAGTTAAACAGGAGCAGCTTGAAGAGCTGGATTT 900  
  
QY 901 TATGCTTTAGGTGAAGTGAATAAGTAAAGTCTTTCACCTGTGGAGAGGGCTAACTGAT 960  
DB 901 TATGCTTTAGGTGAAGTGAATAAGTAAAGTCTTTCACCTGTGGAGAGGGCTAACTGAT 960  
  
QY 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGTTATCCAGGGTGCATAAT 1020  
DB 961 TGGAAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGTTATCCAGGGTGCATAAT 1020  
  
QY 1021 CTGTTTAGAACAGAGGCAAGAATATATAAACAATATTAATTCATTAACTCATTCTTGA 1080  
DB 1021 CTGTTTAGAACAGAGGCAAGAATATATAAACAATATTAATTCATTAACTCATTCTTGA 1080  
  
QY 1081 GAGTCTCTGGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1140  
DB 1081 GAGTCTCTGGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1140  
  
QY 1141 ATCTTCCAAATCCCTATGGTACAAAGATATACGAATGGGTTTCAGTTTCAAGGACAT 1200  
DB 1141 ATCTTCCAAATCCCTATGGTACAAAGATATACGAATGGGTTTCAGTTTCAAGGACAT 1200  
  
QY 1201 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCATTCTGAGGTT 1260  
DB 1201 AAGAAATTAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCATTCTGAGGTT 1260  
  
QY 1261 CTGTTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATCAAGTGAAGTCAAGTCAAGCT 1320  
DB 1261 CTGTTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATCAAGTGAAGTCAAGTCAAGCT 1320  
  
QY 1321 TCATTACAGAAAGAGATTTAGTACTGAAGAGCAGCTTAAGCGGCTGCAAGAGAGAGCTT 1380  
DB 1321 TCATTACAGAAAGAGATTTAGTACTGAAGAGCAGCTTAAGCGGCTGCAAGAGAGAGCTT 1380  
  
QY 1381 TGCATAATCTGTATGGATAGAAATATGCTATCTGTTTGTCTTGTGTCAGATCTAGTC 1440  
DB 1381 TGCATAATCTGTATGGATAGAAATATGCTATCTGTTTGTCTTGTGTCAGATCTAGTC 1440  
  
QY 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAAGTGTCCCATGTGCTACACAGCTCATTACT 1500  
DB 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAAGTGTCCCATGTGCTACACAGCTCATTACT 1500  
  
QY 1501 TTTCAAGCAAAAAATTTTATGTCTTAATCTAATCTATAGTAGGCGATGTTATGTTCTTCT 1560  
DB 1501 TTTCAAGCAAAAAATTTTATGTCTTAATCTAATCTAATCTATAGTAGGCGATGTTATGTTCTTCT 1560  
  
QY 1561 TATTACCTTGATGATGCTGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620  
DB 1561 TATTACCTTGATGATGCTGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620  
  
QY 1621 TAGCATTCTCTACCAAGTAGGAAAAAATGTACATGGCAGTGTCTTGTAGTTGGCAATATA 1680  
DB 1621 TAGCATTCTCTACCAAGTAGGAAAAAATGTACATGGCAGTGTCTTGTAGTTGGCAATATA 1680  
  
QY 1681 ATCTTTGAAATTTCTTGAATTTTTCAGGGTATAGCTGATATATCCATTTTTCCTTACTGTTA 1740  
DB 1681 ATCTTTGAAATTTCTTGAATTTTTCAGGGTATAGCTGATATATCCATTTTTCCTTACTGTTA 1740



QY 1501 TTCAAGCAAAATTTTATGCTTAACTAATCTATAGTAGGCATGTTATGTTGTTCT 1560  
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Db 1561 TATPACCCGTGAATGCTGATGCTGAACGACGCTTTAAGTAATCAGGATGAATCCAT 1620  
QY 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTTATGTTGGCAATATA 1680  
Db 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGCGAGTGTGTTTATGTTGGCAATATA 1680  
QY 1681 ATCTTTGAATTTCTTGAATTTTTCAGGGTATTAGCTGTATTATCCATTTTCTACTGTTA 1740  
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Db 1741 TTTAATTTGAACCATAGACTAAGATAAAGACATCATATATACTGAACAAATGTT 1800  
QY 1801 ATTCACTATATCTATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTAT 1860  
Db 1801 ATTCACTATATCTATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTAT 1860  
QY 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
Db 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA 1920  
QY 1921 ATCTCCCAATCACATAATTTGTTTGTGTAAGAAAGAAATTTGTTCCATGCTGGT 1980  
Db 1921 ATCTCCCAATCACATAATTTGTTTGTGTAAGAAAGAAATTTGTTCCATGCTGGT 1980  
QY 1981 GAAAGATAGAGATTTTGTAGAGTGTGTTGTTGTTTGTAGGATTTCTGTCATTTCT 2040  
Db 1981 GAAAGATAGAGATTTTGTAGAGTGTGTTGTTGTTTGTAGGATTTCTGTCATTTCT 2040  
QY 2041 T 2041  
Db 2041 T 2041

RESULT 15  
US-09-201-932-3  
; Sequence 3, Application US/09201932  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
; FILE REFERENCE: 07891/003004  
; CURRENT APPLICATION NUMBER: US/09/201,932  
; CURRENT FILING DATE: 1998-12-01  
; EARLIER APPLICATION NUMBER: 09/011,356  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: PCT/IB96/01022  
; EARLIER FILING DATE: 1996-08-05  
; EARLIER APPLICATION NUMBER: 08/576,956  
; EARLIER FILING DATE: 1995-12-22  
; EARLIER APPLICATION NUMBER: 08/511,485  
; EARLIER FILING DATE: 1995-08-04  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 2540  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (2540)...(2540)  
; OTHER INFORMATION: N may be any nucleotide

US-09-201-932-3

Query Match 38.0%; Score 1990; DB 16; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAAAGGTGGACAAGTCTTATTTCAAGAGAAGATGACTTTTAAACAGTTTTCGAAGATCT 60  
Db 1 GAAAGGTGGACAAGTCTTATTTCAAGAGAAGATGACTTTTAAACAGTTTTCGAAGATCT 60  
QY 61 AAAAATCTGTGACCTGCAGACATCAATAGGAGAGATTTTGTAGAGATTTTATAGA 120  
Db 61 AAAAATCTGTGACCTGCAGACATCAATAGGAGAGATTTTGTAGAGATTTTATAGA 120  
QY 121 TTAATAAATCTTTTGAATTTTCCAAAGTGTAGTCTGTTTCAAGCATCAACACTGGCAGCA 180  
Db 121 TTAATAAATCTTTTGAATTTTCCAAAGTGTAGTCTGTTTCAAGCATCAACACTGGCAGCA 180  
QY 181 GCAGGTTTCTTTTATCTGTTGAGGAGATACCGTGGGTGCTTTAGTTGTCATGAGCT 240  
Db 181 GCAGGTTTCTTTTATCTGTTGAGGAGATACCGTGGGTGCTTTAGTTGTCATGAGCT 240  
QY 241 GTAGATAGATGCCATATGGAGACTCAGCAGTTGGAGACACAGGAAAGTATCCCAAT 300  
Db 241 GTAGATAGATGCCATATGGAGACTCAGCAGTTGGAGACACAGGAAAGTATCCCAAT 300  
QY 301 TCCAGATTTATCAACGGCTTTTATCTTGAATAATAGTCCACGACGCTTACAAATTTCTGT 360  
Db 301 TCCAGATTTATCAACGGCTTTTATCTTGAATAATAGTCCACGACGCTTACAAATTTCTGT 360  
QY 361 ATCCAGAATGTCAGTCAACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA 420  
Db 361 ATCCAGAATGTCAGTCAACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA 420  
QY 421 GACAGCCATCTGAGACACATCCAGACTATCTTTTGAAGTCTGGCAGGTTGTAGATATA 480  
Db 421 GACAGCCATCTGAGACACATCCAGACTATCTTTTGAAGTCTGGCAGGTTGTAGATATA 480  
QY 481 TCAGACACCATATACCCGAGGAAACCTGCTCATGTATAGTGAAGAGCTAGATTAAGTCC 540  
Db 481 TCAGACACCATATACCCGAGGAAACCTGCTCATGTATAGTGAAGAGCTAGATTAAGTCC 540  
QY 541 TTTTCAAGACTGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
Db 541 TTTTCAAGACTGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTC 600  
QY 601 TACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGTGTTGGTGAAGAACTGAAAT 660  
Db 601 TACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGTGTTGGTGAAGAACTGAAAT 660  
QY 661 TGGGAACCTTGTGATCGTCCCTGGTTCAGAACACAGGACGACTTTTCTTAATTTCTTTT 720  
Db 661 TGGGAACCTTGTGATCGTCCCTGGTTCAGAACACAGGACGACTTTTCTTAATTTCTTTT 720  
QY 721 GTTTTGGCCGGAATCTTAAATATTCGAAGTGAATCTGATGCTGTGAGTTCTTGATAGAA 780  
Db 721 GTTTTGGCCGGAATCTTAAATATTCGAAGTGAATCTGATGCTGTGAGTTCTTGATAGAA 780  
QY 781 TTTCCAAATTCACAAATCTTCCAAAGATCCATCCATGGCAGATTTATGAAGCAGGATC 840  
Db 781 TTTCCAAATTCACAAATCTTCCAAAGATCCATCCATGGCAGATTTATGAAGCAGGATC 840  
QY 841 TTTTACTTTTGGGACATGGATATACCTACAGTTAACAGGACGACTTTCAGAGCTGGATTT 900  
Db 841 TTTTACTTTTGGGACATGGATATACCTACAGTTAACAGGACGACTTTCAGAGCTGGATTT 900  
QY 901 TATGCTTTTGAAGTGAAGTGAATTAAGTCTTCTGCTGGAGGAGGCTTAAGTAT 960  
Db 901 TATGCTTTTGAAGTGAAGTGAATTAAGTCTTCTGCTGGAGGAGGCTTAAGTAT 960  
QY 961 TGGAAAGCCAGTGAAGACCCCTTTGGGAACAACATGCTAAATGGTATCCAGGGTCAAAAT 1020  
Db 961 TGGAAAGCCAGTGAAGACCCCTTTGGGAACAACATGCTAAATGGTATCCAGGGTCAAAAT 1020

Search completed: November 10, 2002, 04:25:20  
Job time : 10495 secs

QY	1021	CTGTTAGAACAGAGGACAGAATATATAAAACAATTCATTAACTCATTCACTTGAG	1080
Db	1021		
QY	1081	GAGTGTCTGGTAAGAACTACTGAGAAACACCACTACTACTAGAGAATTTGATGATACC	1140
Db	1081		
QY	1141	ATCTTCCAAAATCCTATGTTACAGAAGCTATACGAATGGGTTTCAGTTTCAAGGACATT	1200
Db	1141		
QY	1201	AAGAAAATTAATGGAGGAAAAATTCAGATATCTGGAGCAACTATAAATCACTTTGAGGTT	1260
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QY	1261	CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT	1320
Db	1261		
QY	1321	TCATTACAGAAAGAGATTAGTACTGAAGACGAGCTAAGGCGCTGCAAGGAGAGAAGCTT	1380
Db	1321		
QY	1381	TGCAAAATCTGTATGGATAGAAAATTTGCTATCGTTTTTGTCTTCTTGTGGACATCTAGTC	1440
Db	1381		
QY	1441	ACTTGTAAACAATGCTGCTGAAGCAGTTGACAGTGCCCATGTGCTACACAGTCATTA	1500
Db	1441		
QY	1501	TTCAAGCAAAAATTTTATGCTTAACTCTAATCTACTCTATAGTAGGCATGTTATGTTTCT	1560
Db	1501		
QY	1561	TATTACCCCTGATTGAATGTGTGATGTGAACCTGACTTTTAAGTAAATCAGGATTGAATTC	1620
Db	1561		
QY	1621	TAGCATTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTTTAGTTGGCAATATA	1680
Db	1621		
QY	1681	ATCTTTGAATTTCTTGATTTTTCAGGCTATTAGCTGATTAATCCATTTTCTACTGTTA	1740
Db	1681		
QY	1741	TTTAAATTGAACCATAGACTAGAATAAGAAGCATCATACTATACTGAACACAATGTGT	1800
Db	1741		
QY	1801	ATTCATAGTAACTGATTTAATTTCTTAAGTGAAGTGAATTAATCATCTGGATTTTTTAT	1860
Db	1801		
QY	1861	TCCTTTTCAGATAGGCTTAACAATGGAGCTTCTGTATATAAATGTGGAGATTAGAGTTA	1920
Db	1861		
QY	1921	ATCTCCCCAATCACATAATTTGTTTGTGTGAAAAAGGAATAAATGTTCCATGCTGGTG	1980
Db	1921		
QY	1981	GAAAGATAGAGATGTTTATAGAGTTGGTTGTGTTTTAGGATTCGTCCATTTTCT	2040
Db	1981		
QY	2041	T 2041	
Db	2041	T 2041	

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OM nucleic - nucleic search, using sw model

Run on: November 9, 2002, 20:05:26 ; Search time 87 Seconds  
(without alignments)  
9446.005 Million cell updates/sec

Title: US-09-974-592-3  
Perfect score: 5232  
Sequence: 1 gaaaagtggaagtgctca.....tcaaaaaaaaaaaaaaag 5232

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 205966 seqs, 78536166 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 411932

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	314	6.0	315	5	US-09-513-999C-29306
2	151	2.9	190	5	US-09-513-999C-28292
3	85	1.6	237	5	US-09-513-999C-25994
4	79	1.5	237	5	US-09-513-999C-26027
5	79	1.5	276820	6	US-10-271-416-9
6	77	1.5	271	5	US-09-513-999C-20475
7	76	1.5	100267	6	US-10-240-425-1470
8	70	1.3	5574	6	US-09-513-999C-18190
9	69	1.3	212	5	US-09-513-999C-32057
10	69	1.3	231	5	US-09-513-999C-32057
11	69	1.3	133760	6	US-10-240-425-1101
12	69	1.3	304905	6	US-10-271-416-1
13	67	1.3	134292	6	US-10-240-425-1102
14	67	1.3	319608	5	US-09-539-333D-1
15	67	1.3	319608	5	US-09-539-333D-1
16	66	1.3	170	5	US-09-513-999C-27025
17	66	1.3	191	5	US-09-513-999C-22797
18	66	1.3	192	5	US-09-513-999C-22123
19	66	1.3	289	5	US-09-513-999C-19193
20	66	1.3	26928	6	US-10-240-851-6
21	65	1.2	33769	6	US-10-240-851-8
22	63	1.2	137	5	US-09-513-999C-27657
23	63	1.2	278	5	US-09-513-999C-32453
24	61	1.2	215	5	US-09-513-999C-22153
25	61	1.2	445	5	US-09-513-999C-23555
26	60	1.1	1697	6	US-10-240-425-1450

27	60	1.1	8705	6	US-10-240-851-10	Sequence 10, Appl
28	59	1.1	276820	6	US-10-271-416-9	Sequence 9, Appl
c 29	59	1.1	97	5	US-09-513-999C-20263	Sequence 20263, A
c 30	59	1.1	97	5	US-09-513-999C-20264	Sequence 20264, A
c 31	59	1.1	147	5	US-09-513-999C-20249	Sequence 20249, A
c 32	59	1.1	148	5	US-09-513-999C-20098	Sequence 20098, A
c 33	59	1.1	33769	6	US-10-240-851-8	Sequence 8, Appl
c 34	59	1.1	201143	6	US-10-240-425-1099	Sequence 1099, Ap
c 35	57	1.1	196	5	US-09-513-999C-34689	Sequence 34689, A
c 36	56	1.1	152	5	US-09-513-999C-27160	Sequence 27160, A
c 37	55	1.1	133	5	US-09-513-999C-17546	Sequence 17546, A
c 38	55	1.1	199	5	US-09-513-999C-19906	Sequence 19906, A
c 39	54	1.0	239	5	US-09-513-999C-24738	Sequence 24738, A
c 40	54	1.0	311	5	US-09-513-999C-14837	Sequence 14837, A
c 41	54	1.0	16553	6	US-10-264-237-2851	Sequence 2851, Ap
c 42	54	1.0	201143	6	US-10-240-425-1099	Sequence 1099, Ap
c 43	53	1.0	149	5	US-09-513-999C-32581	Sequence 32581, A
c 44	53	1.0	167	5	US-09-513-999C-20746	Sequence 20746, A
c 45	53	1.0	202	5	US-09-513-999C-17350	Sequence 17350, A

ALIGNMENTS

RESULT 1  
US-09-513-999C-29306  
; Sequence 29306, Application US/09513999C  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 29306  
; LENGTH: 315  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-29306

Query Match	6.0%;	Score 314;	DB 5;	Length 315;
Best local Similarity	100.0%;	Pred. No. 6.3e-102;	Mismatches 0;	Indels 0;
Matches 314;	Conservative 0;			
QY 4005	CATTAAATTCCTCTAAAACTTGATGTTAGAGTTAAGCAAGACTTTTCTTCTCTCT	4064		
Db 1	CATTAAATTCCTCTAAAACTTGATGTTAGAGTTAAGCAAGACTTTTCTTCTCTCT	60		
QY 4065	CCATGAGTTGTGAATTTAATGCACACCGCTGATGGGTAAACAAGTTATTTAAGAAT	4124		
Db 61	CCATGAGTTGTGAATTTAATGCACACCGCTGATGGGTAAACAAGTTATTTAAGAAT	120		
QY 4125	TCGTTAGAAATGCTGTGCTTCAAGTTCCTTAAATCAGTCAGCACTCCCACTTCTAATCA	4184		
Db 121	TCGTTAGAAATGCTGTGCTTCAAGTTCCTTAAATCAGTCAGCACTCCCACTTCTAATCA	180		
QY 4185	AATTTTGGAGACTTAAACAGCACTTTCGTGTGTGTTTGAACATATATAAAGACCGGATCTTT	4244		
Db 181	AATTTTGGAGACTTAAACAGCACTTTCGTGTGTGTTTGAACATATATAAAGACCGGATCTTT	240		
QY 4245	TCCATCTAATTCGCAAAAATTTGATCATTTGCCAAAGTCAAACTATAGCATATCCAAAT	4304		
Db 241	TCCATCTAATTCGCAAAAATTTGATCATTTGCCAAAGTCAAACTATAGCATATCCAAAT	300		
QY 4305	CTTTTCCCTCCCTCC 4318			
Db 301	CTTTTCCCTCCCTCC 314			

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RESULT 2
US-09-513-999C-28292
; Sequence 28292, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 28292
; LENGTH: 190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 173
; OTHER INFORMATION: b=c or g or t
US-09-513-999C-28292

Query Match          2.9%; Score 151; DB 5; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2121 ATACTATCGAGCCAAACATGCTACTGACATGGAAGATGTCAAAGATATGTTAAAGTGTAAAA 2180
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Db 1 ATACTATCGAGCCAAACATGCTACTGACATGGAAGATGTCAAAGATATGTTAAAGTGTAAAA 60

QY 2181 TGCAAGTGGCAAAACACTATGATCTAGTCGAGCCAGATCAAGATATGTTAAATA 2240
|||||
Db 61 TGCAAGTGGCAAAACACTATGATCTAGTCGAGCCAGATCAAGATATGTTAAATA 120

QY 2241 TGCAATAGACAAAGATTTGGAAAGATATAC 2271
|||||
Db 121 TGCAATAGACAAAGATTTGGAAAGATATAC 151

RESULT 3
US-09-513-999C-25994/c
; Sequence 25994, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 25994
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-25994

Query Match          1.6%; Score 85; DB 5; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4947 TGCTTCACGCTGTAATCCAGCAGCTTTGGAGGCTGAGGAGGTGATCAGCAGGTCTCAG 5006
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Db 124 TGCTTCACGCTGTAATCCAGCAGCTTTGGAGGCTGAGGAGGTGATCAGCAGGTCTCAG 65

QY 5007 GAGATCGAGACCATCCTGGCTAACA 5031
|||||
Db 507 GAGATCGAGACCATCCTGGCTAACA 40

RESULT 4
US-09-513-999C-26027/c
; Sequence 26027, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 26027
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 119
; OTHER INFORMATION: r=a or g
; NAME/KEY: misc_feature
; LOCATION: 139
; OTHER INFORMATION: r=a or g
; NAME/KEY: misc_feature
; LOCATION: 146
; OTHER INFORMATION: m=a or c
US-09-513-999C-26027

Query Match          1.5%; Score 79; DB 5; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4953 ACGCCTGTAATCCAGCAGCTTTGGAGGCTGAGGAGGTGATCAGCAGGTCTCAGGAGATC 5012
|||||
Db 118 ACGCCTGTAATCCAGCAGCTTTGGAGGCTGAGGAGGTGATCAGCAGGTCTCAGGAGATC 59

QY 5013 GAGACCATCCTGGCTAACA 5031
|||||
Db 58 GAGACCATCCTGGCTAACA 40

RESULT 5
US-10-271-416-9/c
; Sequence 9, Application US/10271416
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; APPLICANT: Little, Randall D.
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Dupuis, Josee
; APPLICANT: Del Maestro, Richard G.
; APPLICANT: Allen, Kristina
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: 2976-4045
; CURRENT APPLICATION NUMBER: US/10/271,416
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,424
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 276820
; TYPE: DNA
; ORGANISM: Homo sapien
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; FEATURE:
; NAME/KEY: conflict
; LOCATION: (167043)...(167043)
; OTHER INFORMATION: Y-C or T
US-10-271-416-9

Query Match          1.5%; Score 79; DB 6; Length 276820;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5084 GGGCGCCTGTAGTCCACACTACTCGGGAGGCTGAGGCAGGAGAAATGGTGTGAACCCGGGA 5143
Db 276166 GGGCGCCTGTAGTCCACACTACTCGGGAGGCTGAGGCAGGAGAAATGGTGTGAACCCGGGA 276107

Qy 5144 GGCAGAGCTTCAGTGAGC 5162
Db 276106 GGCAGAGCTTCAGTGAGC 276088

RESULT 6
US-09-513-999C-20475/c
; Sequence 20475, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 20475
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 261
; OTHER INFORMATION: s-g or c
US-09-513-999C-20475

Query Match          1.5%; Score 77; DB 5; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5062 AAAATTAGCGGGCGTGTGGCGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCA 5121
Db 148 AAAATTAGCGGGCGTGTGGCGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCA 89

Qy 5122 GGAGAAATGGTGTGAACC 5138
Db 88 GGAGAAATGGTGTGAACC 72

RESULT 7
US-10-240-425-1470/c
; Sequence 1470, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 17963
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1470
; LENGTH: 100267
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U89337
US-10-240-425-1470

Query Match          1.5%; Score 76; DB 6; Length 100267;
Best Local Similarity 100.0%; Pred. No. 5.8e-19;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4983 GAGCGAGTGGATCACGAGGTGAGGATCGAGACCATCTCGCTTAACACGGTGAACCC 5042
Db 18022 GAGCGAGTGGATCACGAGGTGAGGATCGAGACCATCTCGCTTAACACGGTGAACCC 17963

Qy 5043 CGTCTCTACTAAAAA 5058
Db 17962 CGTCTCTACTAAAAA 17947

RESULT 8
US-10-240-425-396/c
; Sequence 396, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 396
; LENGTH: 5574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF055481
US-10-240-425-396

Query Match          1.3%; Score 70; DB 6; Length 5574;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5077 TGGTGGCGGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAAATGGTGTGAA 5136
Db 1178 TGGTGGCGGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAAATGGTGTGAA 1119

Qy 5137 CCCGGGAGGC 5146
Db 1118 CCCGGGAGGC 1109

RESULT 9
US-09-513-999C-18190
; Sequence 18190, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
```

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; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1470
; LENGTH: 100267
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U89337
US-10-240-425-1470

Query Match          1.5%; Score 76; DB 6; Length 100267;
Best Local Similarity 100.0%; Pred. No. 5.8e-19;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4983 GAGCGAGTGGATCACGAGGTGAGGATCGAGACCATCTCGCTTAACACGGTGAACCC 5042
Db 18022 GAGCGAGTGGATCACGAGGTGAGGATCGAGACCATCTCGCTTAACACGGTGAACCC 17963

Qy 5043 CGTCTCTACTAAAAA 5058
Db 17962 CGTCTCTACTAAAAA 17947

RESULT 8
US-10-240-425-396/c
; Sequence 396, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 396
; LENGTH: 5574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF055481
US-10-240-425-396

Query Match          1.3%; Score 70; DB 6; Length 5574;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5077 TGGTGGCGGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAAATGGTGTGAA 5136
Db 1178 TGGTGGCGGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAAATGGTGTGAA 1119

Qy 5137 CCCGGGAGGC 5146
Db 1118 CCCGGGAGGC 1109

RESULT 9
US-09-513-999C-18190
; Sequence 18190, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
```



```
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 18190
; LENGTH: 212
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 132
; OTHER INFORMATION: m-a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 184
; OTHER INFORMATION: w-a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 200
; OTHER INFORMATION: w-a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 202
; OTHER INFORMATION: k-g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 203
; OTHER INFORMATION: y-c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 212
; OTHER INFORMATION: r-a or g
US-09-513-999C-18190

Query Match 1.3%; Score 69; DB 5; Length 212;
Best Local Similarity 100.0%; Pred. No. 7.2e-16;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5062 AAAATTAGCGGCGGTGGTGGCGGCGCTGTAGTCCAGCTACTCCAGCTACTCGGAGGCTGAGGCA 5121
|||||
DB 18 AAAATTAGCGGCGGTGGTGGCGGCGCTGTAGTCCAGCTACTCCAGCTACTCGGAGGCTGAGGCA 77

QY 5122 GGAGATGG 5130
|||||
DB 78 GGAGATGG 86

RESULT 10
US-09-513-999C-32057
; Sequence 32057, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 32057
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: 215
; OTHER INFORMATION: s-g or c
US-09-513-999C-32057

Query Match 1.3%; Score 69; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.1e-16;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4989 GGTGGATCAGGAGGTGAGGATCGAGACCATCTGGCTAACACGGTGAACCCCGTCTC 5048
|||||
DB 22 GGTGGATCAGGAGGTGAGGATCGAGACCATCTGGCTAACACGGTGAACCCCGTCTC 81

QY 5049 TACTAAAAA 5057
|||||
DB 82 TACTAAAAA 90

RESULT 11
US-10-240-425-1101
; Sequence 1101, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Bolland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1101
; LENGTH: 133760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AL031737
US-10-240-425-1101

Query Match 1.3%; Score 69; DB 6; Length 133760;
Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5062 AAAATTAGCGGCGGTGGTGGCGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGCA 5121
|||||
DB 120084 AAAATTAGCGGCGGTGGTGGCGGCGCTGTAGTCCAGCTACTCGGAGGCTGAGGCA 120143

QY 5122 GGAGATGG 5130
|||||
DB 120144 GGAGATGG 120152

RESULT 12
US-10-271-416-1
; Sequence 1, Application US/10271416
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; APPLICANT: Little, Randall D.
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Dupuis, Josee
; APPLICANT: Del Mastro, Richard G.
; APPLICANT: Allen, Kristina
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: 2976-4045
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; CURRENT APPLICATION NUMBER: US/10/271,416  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/328,424  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 304905  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-271-416-1

Query Match 1.3%; Score 69; DB 6; Length 304905;  
Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5062 AAAATTAGCGGCGTGTGGGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCA 5121  
|||||  
Db 25099 AAAATTAGCGGCGTGTGGGGCGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCA 25158  
|||||  
Qy 5122 GGAGAAATGG 5130  
|||||  
Db 25159 GGAGAAATGG 25167  
|||||

RESULT 13  
US-10-240-425-1102  
; Sequence 1102, Application US/10240425  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Boland, Joseph F.  
; APPLICANT: Lord, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240,425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193,446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1102  
; LENGTH: 134292  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. AL031983  
US-10-240-425-1102

Query Match 1.3%; Score 67; DB 6; Length 134292;  
Best Local Similarity 100.0%; Pred. No. 7.8e-16;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4952 GGATCAGGTCAGGAGTCGAGACCATCTGGCTACACGGTGAACCCCGTCTCTAC 5051  
|||||  
Db 113318 GGATCAGGTCAGGAGTCGAGACCATCTGGCTACACGGTGAACCCCGTCTCTAC 113377  
|||||  
Qy 5052 TAAAAAA 5058  
|||||  
Db 113378 TAAAAAA 113384  
|||||

RESULT 14  
US-09-539-333D-1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya

; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Bihain, Bernard  
; APPLICANT: Essioux, Laurent  
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS  
; FILE REFERENCE: GENSET.04TAUS  
; CURRENT APPLICATION NUMBER: US/09/539,333D  
; CURRENT FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: US 60/126,903  
; PRIOR FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: US 60/131,971  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: US 60/132,065  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: US 60/143,928  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: US 60/145,915  
; PRIOR FILING DATE: 1999-07-27  
; PRIOR APPLICATION NUMBER: US 60/146,453  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: US 60/146,452  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: US 60/162,288  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: US 09/416,384  
; PRIOR FILING DATE: 1999-10-12  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: Patent.pm  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 110222  
; OTHER INFORMATION: polymorphic base G or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 111978  
; OTHER INFORMATION: polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 112468  
; OTHER INFORMATION: polymorphic base G or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 117324..117327  
; OTHER INFORMATION: deletion ACTT  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 118972  
; OTHER INFORMATION: polymorphic base C or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 119160..119161  
; OTHER INFORMATION: deletion TT  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 119316  
; OTHER INFORMATION: polymorphic base C or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 119321  
; OTHER INFORMATION: polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 119526  
; OTHER INFORMATION: polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 120573  
; OTHER INFORMATION: polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 121527  
; OTHER INFORMATION: polymorphic base A or C  
; FEATURE:  
; NAME/KEY: allele

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/ LOCATION: 126105
/ OTHER INFORMATION: polymorphic base C or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 129789
/ OTHER INFORMATION: polymorphic base C or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 130777
/ OTHER INFORMATION: polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 136942..136944
/ OTHER INFORMATION: deletion ATT
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 143839
/ OTHER INFORMATION: polymorphic base A or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 146668
/ OTHER INFORMATION: polymorphic base C or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 147281
/ OTHER INFORMATION: polymorphic base C or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 147505
/ OTHER INFORMATION: polymorphic base G or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 148183
/ OTHER INFORMATION: deletion T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 148372
/ OTHER INFORMATION: polymorphic base A or C
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 149012
/ OTHER INFORMATION: polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 149113
/ OTHER INFORMATION: polymorphic base C or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 151637
/ OTHER INFORMATION: polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 151748
/ OTHER INFORMATION: deletion G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 151769
/ OTHER INFORMATION: polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 151847
/ OTHER INFORMATION: polymorphic base C or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 152691
/ OTHER INFORMATION: polymorphic base A or C
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 152766
/ OTHER INFORMATION: polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 153046
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/ OTHER INFORMATION: polymorphic base C or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 153123
/ OTHER INFORMATION: polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 153925
/ OTHER INFORMATION: polymorphic base C or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 153977
/ OTHER INFORMATION: polymorphic base G or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 154502
/ OTHER INFORMATION: polymorphic base C or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 154677
/ OTHER INFORMATION: polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 154879
/ OTHER INFORMATION: polymorphic base C or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 154918
/ OTHER INFORMATION: polymorphic base G or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 155802
/ OTHER INFORMATION: polymorphic base C or T
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 156448
/ OTHER INFORMATION: polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 157238
/ OTHER INFORMATION: polymorphic base A or C
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 157897
/ OTHER INFORMATION: polymorphic base A or G
/ FEATURE:
/ NAME/KEY: allele
/ LOCATION: 158172
/ OTHER INFORMATION: polymorphic base A or G
/ FEATURE:
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Query Match 1.3%; Score 67; DB 5; Length 319608;
Best Local Similarity 100.0%; Pred.No.6.4e-16;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5062 AAATATTAGCGGGCGGTGGCGGCGCCTGTAGTCCAGCTACTCGGAGGCTGAGGCA 5121
|||||
Db 276617 AAATATTAGCGGGCGGTGGCGGCGCCTGTAGTCCAGCTACTCGGAGGCTGAGGCA 276676
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QY 5122 GGAGAAAT 5128
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Db 276677 GGAGAAAT 276683
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RESULT 15
US-09-539-333D-1
; Sequence 1, Application US/09539333D
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueret, Lydie
; APPLICANT: Bihain, Bernard
```

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; APPLICANT: Essloux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSER.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 319608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31..1107
; OTHER INFORMATION: 5'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1108..1289
; OTHER INFORMATION: exon A g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 14877..14920
; OTHER INFORMATION: exon B g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 18778..18862
; OTHER INFORMATION: exon Bbis g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 25593..25740
; OTHER INFORMATION: exon C g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 29388..29502
; OTHER INFORMATION: exon D g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 29967..30282
; OTHER INFORMATION: exon E g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 64666..64812
; OTHER INFORMATION: exon F g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 65505..65853
; OTHER INFORMATION: exon G g35018 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 65854..67854
; OTHER INFORMATION: 3'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 94124..94964
; OTHER INFORMATION: exon g35017
;
; FEATURE:
; NAME/KEY: exon
; LOCATION: 201188..201234
; OTHER INFORMATION: exon S g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 214676..214793
; OTHER INFORMATION: exon T g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215702..215746
; OTHER INFORMATION: exon U g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216836..216915
; OTHER INFORMATION: exon V g35030 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 213818..215818
; OTHER INFORMATION: 3'regulatory region g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215819..215941
; OTHER INFORMATION: exon R complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215819..215975
; OTHER INFORMATION: exon Rbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216661..216952
; OTHER INFORMATION: exon Qbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216661..217061
; OTHER INFORMATION: exon Q complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 217027..217061
; OTHER INFORMATION: exon Q1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 229647..229742
; OTHER INFORMATION: exon X complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 230408..230721
; OTHER INFORMATION: exon P complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231272..231412
; OTHER INFORMATION: exon Obis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231787..231880
; OTHER INFORMATION: exon O2 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231870..231879
; OTHER INFORMATION: exon O1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 234174..234321
; OTHER INFORMATION: exon O complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 237406..237428
; OTHER INFORMATION: exon Nbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 239719..239807
; OTHER INFORMATION: exon N2 complement g34872 gene
; FEATURE:
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; NAME/KEY: exon
; LOCATION: 239719..239853
; OTHER INFORMATION: exon N complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240569
; OTHER INFORMATION: exon M1117 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240596
; OTHER INFORMATION: exon M1090 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240617
; OTHER INFORMATION: exon M1069 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240644
; OTHER INFORMATION: exon M52 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240824
; OTHER INFORMATION: exon M862 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..240994
; OTHER INFORMATION: exon M692 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240528..241685
; OTHER INFORMATION: exon M1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 240800..240993
; OTHER INFORMATION: exon M51 complement g34872 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 241686..243685
; OTHER INFORMATION: 5'regulatory region g34872 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 290652..292652
; OTHER INFORMATION: 3'regulatory region g34665 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 292653..292841
; OTHER INFORMATION: exon B complement g34665 gene
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Query Match 1.3%; Score 67; DB 5; Length 319608;
Best Local Similarity 100.0%; Pred. No. 6.4e-16;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5062 AAAATTAGCGGGCGTGGTGGCGGGCGCTGTAGTCCCGAGCTACTCGGGAGGCTGAGGCA 5121
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Db 276617 AAAATTAGCGGGCGTGGTGGCGGGCGCTGTAGTCCCGAGCTACTCGGGAGGCTGAGGCA 276676
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QY 5122 GGAGAAAT 5128
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Db 276677 GGAGAAAT 276683
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Search completed: November 10, 2002, 05:25:04
Job time : 3430 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using -sw model

Run on: November 9, 2002, 19:46:46 ; Search time 6593 Seconds  
(without alignments)  
12852.235 Million cell updates/sec.

Title: US-09-974-592-3

Perfect score: 5232

Sequence: 1 gaaagagtgcacagtctca.....tcaaaaaaaaaaaaaaaag 5232

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_Other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
c 1	641	12.3	757	14	BQ007511	BQ007511 UI-H-ED1-
c 2	571	10.9	822	12	BG502660	BG502660 602549490
c 3	567	10.8	1041	13	BM459898	BM459898 AGENCOURT
c 4	551	10.5	784	9	AI628066	AI628066 ty84b02.x
c 5	469	9.0	529	9	AL713196	AL713196 DKFZp686M
c 6	455	8.7	691	14	BM990097	BM990097 UI-H-D10-

7	450	8.6	537	12	BG616695	BG616695 602614908
c 8	434	8.3	462	12	BF510268	BF510268 UI-H-BI4-
c 9	432	8.3	943	12	BG164322	BG164322 602341372
c 10	422	8.1	472	9	AI277821	AI277821 qm60e01.x
c 11	406	7.8	406	9	AI299965	AI299965 qo24a11.x
c 12	406	7.8	508	10	AW665401	AW665401 h190c08.x
c 13	405	7.7	409	10	BE222433	BE222433 hv90g11.x
c 14	398	7.6	413	9	AI681542	AI681542 tx47e09.x
c 15	389	7.4	707	13	BI823020	BI823020 603039619
c 16	371	7.1	447	9	AI418337	AI418337 tg48a12.x
c 17	368	7.0	648	13	BI094339	BI094339 602860253
c 18	366	7.0	446	12	BF754025	BF754025 CM2-CT500
c 19	357	6.8	681	9	AL138255	AL138255 DKF2p547E
c 20	336	6.4	587	10	AW750285	AW750285 PMO-BT058
c 21	320	6.1	360	10	BE220552	BE220552 ht98a01.x
c 22	303	5.8	693	10	BE380045	BE380045 601159359
c 23	296	5.7	852	14	BQ423165	BQ423165 AGENCOURT
c 24	288	5.5	698	12	BG617067	BG617067 602616141
c 25	245	4.7	461	9	AA115728	AA115728 z186h12.r
c 26	243	4.6	885	12	BE896438	BE896438 601439815
c 27	230	4.4	230	9	AA987840	AA987840 cq93f09.s
c 28	230	4.4	288	14	F08325	F08325 HSCZOG051.n
c 29	228	4.4	386	10	AW673379	AW673379 ba33e09.y
c 30	227	4.3	1177	14	BM805359	BM805359 AGENCOURT
c 31	210	4.0	536	9	AU123207	AU123207 AU123207
c 32	207	4.0	494	14	BQ369513	BQ369513 RC3-GN007
c 33	204	3.9	255	9	AA345330	AA345330 EST51334
c 34	203	3.9	320	10	AW807831	AW807831 MR4-ST009
c 35	176	3.4	465	10	AW675725	AW675725 ba33e09.x
c 36	174	3.3	535	9	AI861853	AI861853 tz91a08.x
c 37	172	3.3	337	14	H64979	H64979 yu66a10.s1
c 38	167	3.2	216	12	BE813985	BE813985 QV3-BN004
c 39	165	3.2	270	12	BE815593	BE815593 PMO-BN016
c 40	163	3.1	308	9	AI873852	AI873852 wu42e07.x
c 41	162	3.1	716	10	AV706807	AV706807 AV706807
c 42	153	2.9	284	9	AA295472	AA295472 EST100639
c 43	149	2.8	993	14	BQ233403	BQ233403 AGENCOURT
c 44	145	2.8	235	14	241329	241329 HSCZOG052.n
c 45	144	2.8	304	9	AI914443	AI914443 wd49b11.x

#### ALIGNMENTS

RESULT 1  
BQ007511/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

757 bp  
linear  
EST 26-MAR-2002  
UI-H-ED1-ayb-b-04-0-UI.s1 NCI\_CGAP\_ED1 Homo sapiens cDNA clone  
IMAGE:5836323 3', mRNA sequence.

BQ007511  
BQ007511.1  
GI:19732411

EST.  
human.  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 757)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Dr. Jose Mercuende  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Seq primer: M13 FORWARD  
POLYA-Yes.  
Location/Qualifiers  
1. 757

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/db_xref="taxon:9606"
/clone="IMAGE:5836323"
/clone_lib="NCI_CGAP_ED1"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site.1: Ecor I;
Site.2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an Ecor I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (drr)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_LIB=UI-H-ED1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CCTCAAGCT"
BASE COUNT 257 a 141 c 105 g 254 t
ORIGIN
Query Match 12.3%; Score 641; DB 14; Length 757;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1288 AAGACAGTATGCAAGTACAGTTCATACAGAAAGAGATTAGTACTGAA 1347
DB 713 AAAGACAGTATGCAAGTACAGTTCATACAGAAAGAGATTAGTACTGAA 654
QY 1348 GACAGCTAGGCGCTGCAAGAGGAGAGCTTGCAGAAATCTGTATGATGAAATATT 1407
DB 653 GACAGCTAGGCGCTGCAAGAGGAGAGAGCTTGCAGAAATCTGTATGATGAAATATT 594
QY 1408 GCTATGCTTTTCTTCTGTGGACATCTAGTACATTTGTAACAATGTGCTGAAGCAGTT 1467
DB 593 GCTATGCTTTTCTTCTGTGGACATCTAGTACATTTGTAACAATGTGCTGAAGCAGTT 534
QY 1468 GACAAGTGCCCATGTGTACACAGTCATTTTCAAGCAAAAAATTTTATGTCTTAA 1527
DB 533 GACAAGTGCCCATGTGTGTACACAGTCATTTTCAAGCAAAAAATTTTATGTCTTAA 474
QY 1528 TCTAACTCTATAGGCGATGTTATGTTCTTATACCTGATTCGAATGTGTATGTG 1587
DB 473 TCTAACTCTATAGGCGATGTTATGTTCTTATACCTGATTCGAATGTGTATGTG 414
QY 1588 AACTGACTTTAAGTAACTAGGATTGAATCCATTAGCATTTGCTACCAAGTAGGAAAAA 1647
DB 413 AACTGACTTTAAGTAACTAGGATTGAATCCATTAGCATTTGCTACCAAGTAGGAAAAA 354
QY 1648 AATGTACATGGCAGTGTGTTAGTGGCAATATAATCTTTGAAATTTCTGATTTTCAGGG 1707
DB 353 AATGTACATGGCAGTGTGTTAGTGGCAATATAATCTTTGAAATTTCTGATTTTCAGGG 294
QY 1708 TATTAGCTGATTTATCCATTTTCTTACTGTTATTTAATTTGAACCATAGACTAAGAATA 1767
DB 293 TATTAGCTGATTTATCCATTTTCTTACTGTTATTTAATTTGAACCATAGACTAAGAATA 234
QY 1768 AGAAGCATCATACTAATACTGAACACAATGTGTATTCATAGTATCTGATTTAATTTCTA 1827
DB 233 AGAAGCATCATACTAATACTGAACACAATGTGTATTCATAGTATCTGATTTAATTTCTA 174
QY 1828 AGTGAAGTGAATTAATCATCTGGAATTTTATTTCTTTTCAGATAGGCTTAACAAATGGA 1887
DB 173 AGTGAAGTGAATTAATCATCTGGAATTTTATTTCTTTTCAGATAGGCTTAACAAATGGA 114
QY 1888 GCTTTCTGTATATAATGTGGAGATTAGAGTTAATCTCCCC 1928
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Db 113 GCTTCTGTATATAAATGTGGAGATTAGACTTAATCTCCCC 73
RESULT 2
BG502660 822 bp mRNA linear EST 27-MAR-2001
LOCUS 602549490F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4657102 5',
DEFINITION mRNA sequence.
ACCESSION BG502660
VERSION BG502660.1 GI:13464177
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 822)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1449 row: C column: 23
High quality sequence stop: 670.
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4657102"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: Testis; Vector: pDNR-LIB (Clontech); Site.1:
SfiI (ggccattggcc); Site.2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGGCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 236 a 161 c 201 g 222 t 2 others
ORIGIN
Query Match 10.9%; Score 571; DB 12; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 184 GGTTTTCTTTATACTGTTGAAGGAGATACCGTCGCTGCTTTTAGTGTCTATGCGAGCTGTA 243
DB 1 GGTTTTCTTTATACTGTTGAAGGAGATACCGTCGCTGCTTTTAGTGTCTATGCGAGCTGTA 60
QY 244 GATAGATGCAATATATGGAGACTCAGCAGTTGGGAAGACACAGAGAAAGTATCCCCAAATTGC 303
DB 61 GATAGATGCAATATATGGAGACTCAGCAGTTGGGAAGACACAGAGAAAGTATCCCCAAATTGC 120
QY 304 AGATTTATCAAGCGCTTTTATCTTGAATAATAGTGCACGAGCTCTACAAATTCGTGATC 363
DB 121 AGATTTATCAAGCGCTTTTATCTTGAATAATAGTGCACGAGCTCTACAAATTCGTGATC 180
QY 364 CAGAATGGTTCAGTACAAAGTGTGAAACTATCTGGGAGCAGAGATCATTTTGGCTTAGAC 423
DB 181 CAGAATGGTTCAGTACAAAGTGTGAAACTATCTGGGAGCAGAGATCATTTTGGCTTAGAC 240
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QY 424 AGCCATCTGAGACACATGACGACTATCTTTTGAGAACTGGCAGGTTGTAGATATATCA 483
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Db 241 AGCCATCTGAGACACATGACGACTATCTTTTGAGAACTGGCAGGTTGTAGATATATCA 300
QY 484 GACACATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAGTCTCTTT 543
|||||
Db 301 GACACATATACCCGAGGAACCTGCCATGTATAGTGAAGAGCTAGATTAAGTCTCTTT 360
QY 544 CAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTCTAC 603
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Db 361 CAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTCTGGACTCTAC 420
QY 604 TACACAGTATTGGTGACCAAGTGCAGTCTTTTGTGTGGTGGAAACTGAAAAATTGG 663
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Db 421 TACACAGTATTGGTGACCAAGTGCAGTCTTTTGTGTGGTGGAAACTGAAAAATTGG 480
QY 664 GAACCTTGATGTCGTCCTGGTTCAGACACAGCGGACACTTTCCTAAATGCTTCTTGT 723
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Db 481 GAACCTTGATGTCGTCCTGGTTCAGACACAGCGGACACTTTCCTAAATGCTTCTTGT 540
QY 724 TTGGGCGGAATCTTAATATTGGAAGTGAAT 754
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Db 541 TTGGGCGGAATCTTAATATTGGAAGTGAAT 571

RESULT 3
BM459898 1041 bp mRNA linear EST 05-FEB-2002
AGENCY: NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532247
5', mRNA sequence.
BM459898
BM459898.1 GI:18508938
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12215 row: d column: 08
High quality sequence stop: 567.
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_71"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
BASE COUNT 297 a 208 c 266 g 269 t 1 others
ORIGIN
Query Match 10.8%; Score 567; DB 13; Length 1041;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 617; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAAAGGTGGACAGTCTCTATTTCAGAGAGAGATGACATTTTAAACAGTTTGAAGATCT 60
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Db 34 GAAAGGTGGACAGTCTCTATTTCAGAGAGAGATGACATTTTAAACAGTTTGAAGATCT 93
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QY 61 AAAACTTGTTGTACCTGCAGACATCAATAAGGAAGAAGAAATTTGTAGAAGAGTTTATAGA 120
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Db 94 AAAACTTGTTGTACCTGCAGACATCAATAAGGAAGAAGAAATTTGTAGAAGAGTTTATAGA 153
QY 121 TTAATAAATTTTGGTAAATTTTCCAAAGTGGTAGTCCCTGTTTTCAGCATCAACACTGGCACA 180
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Db 154 TTAATAAATTTTGGTAAATTTTCCAAAGTGGTAGTCCCTGTTTTCAGCATCAACACTGGCACA 213
QY 181 GCAGGGTCTTCTTATATCTGCTGAAGAGATACCGTCCGCTGCTTTAGTTGTCTATGAGCT 240
|||||
Db 214 GCAGGGTCTTCTTATATCTGCTGAAGAGATACCGTCCGCTGCTTTAGTTGTCTATGAGCT 273
QY 241 GTAGATAGATGCAATATATGGAGACTCAGCAGTTTGAAGACACACAGGAAAGTATATCCCAAT 300
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Db 274 GTAGATAGATGCAATATATGGAGACTCAGCAGTTTGAAGACACACAGGAAAGTATATCCCAAT 333
QY 301 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTCCACGAGTCTACAAATTCGTGT 360
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Db 334 TGCAGATTTATCAACGGCTTTTATCTTGAATAATAGTCCACGAGTCTACAAATTCGTGT 393
QY 361 ATCCAGAAATGGTCACTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA 420
|||||
Db 394 ATCCAGAAATGGTCACTACAAAGTTGAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA 453
QY 421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAAGAACTGGGAGGTTGTAGATATA 480
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Db 454 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAAGAACTGGGAGGTTGTAGATATA 513
QY 481 TCAGACACCATATATACCCGAGGAACCTGCCATGTATAGTGAAGAACTAGATTAAGATCC 540
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Db 514 TCAGACACCATATATACCCGAGGAACCTGCCATGTATAGTGAAGAACTAGATTAAGATCC 573
QY 541 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTACAAAGTCTGTCAGCTC 600
|||||
Db 574 TTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTACAAAGTCTGTCAGCTC 633
QY 601 TACTACACAGGTATTGGT 618
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Db 634 TACTACACAGGTATTGGT 651

RESULT 4
AI628066/c
LOCUS
DEFINITION
AI628066
AI628066.1 GI:4664866
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 784)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor gene index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Distribution: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -400P from Gibco
High quality sequence stop: 466
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POLYA=No.

FEATURES  
source

Location/Qualifiers  
1..784

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/clone="IMAGE:2285739"  
/clone\_lib="NCI\_CGAP\_Kid11"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP\_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-132391, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 266 a 152 c 106 g 255 t 5 others  
ORIGIN

Query Match 10.5%; Score 551; DB 9; Length 784;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1419 TGTTCTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCC 1478  
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Db 563 TGTTCTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCC 504  
QY 1479 CATGTGCTACAGACATCTACATTTCAAGCAAAAAATTTTATGCTTAACTACTCTAT 1538  
|||||  
Db 503 CATGTGCTACAGACATCTACTTCAAGCAAAAAATTTTATGCTTAACTACTCTAT 444  
QY 1539 AGTAGCAGTGTATGTGTCTTATTACCTGATTGAATGTGTGATGTAAGTCACTTTA 1598  
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Db 443 AGTAGCAGTGTATGTGTCTTATTACCTGATTGAATGTGTGATGTAAGTCACTTTA 384  
QY 1599 AGTAATCAGGATTGAATCCATTAGCATTTGTACCAAGTAGGAAAAAATGTACATGG 1658  
|||||  
Db 383 AGTAATCAGGATTGAATCCATTAGCATTTGTACCAAGTAGGAAAAAATGTACATGG 324  
QY 1659 CAGTGTGTAGTTGGCAATATAATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTA 1718  
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Db 323 CAGTGTGTAGTTGGCAATATAATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTA 264  
QY 1719 TTATCCATTTTTTTTACTGTTATTAATTTGAACCATAGACTAAGAAATGAAGCATCAT 1778  
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Db 263 TTATCCATTTTTTTTACTGTTATTAATTTGAACCATAGACTAAGAAATGAAGCATCAT 204  
QY 1779 ACTATACTGAACACAAATGTGATTATCATAGTATATCTGATTAATTTCTAAGTGAAGTGA 1838  
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Db 203 ACTATACTGAACACAAATGTGATTATCATAGTATATCTGATTAATTTCTAAGTGAAGTGA 144  
QY 1839 ATTAATCATCTGGATTTTTTATCTTTTCAGATAGGCTTAAACAATGGAGCTTTCTGTAT 1898  
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Db 143 ATTAATCATCTGGATTTTTTATCTTTTCAGATAGGCTTAAACAATGGAGCTTTCTGTAT 84  
QY 1899 ATAAATGTGGAGATTAGCTTAACTCCCAATACATAATTTGTTTGTGTGAAAAAGG 1958  
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Db 83 ATAAATGTGGAGATTAGCTTAACTCCCAATACATAATTTGTTTGTGTGAAAAAGG 24  
QY 1959 AATAAATTTGTT 1969  
|||||  
Db 23 AATAAATTTGTT 13

RESULT 5  
AL713196  
LOCUS AL713196 529 bp mRNA linear EST 22-MAR-2002  
DEFINITION DKFP686M1895\_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
ACCESSION DKFP686M1895 5', mRNA sequence.  
VERSION AL713196  
AL713196.1 GI:19696552

EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 529)  
Bloeker, H., Boecher, M., Brandt, P., Mewes, W., Weill, B. and Wiemann  
S.  
EST (Bloeker, H., Boecher, M., Brandt, P., Mewes, H.W., Weill, B. and  
Wiemann, S.)  
Unpublished (1999)  
Contact: Bloeker H  
MIPS  
Am Klopferstr. 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by GBF (National Research Centre for Biotechnology Ltd.,  
Braunschweig/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFP686M1895) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.  
Location/Qualifiers  
1..529  
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/db\_xref="taxon:9606"  
/clone="DKFP686M1895"  
/clone\_lib="686 (synonym: hlcc3)"  
/tissue\_type="human skeletal muscle"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Vector: pTriplex2; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA collection"  
BASE COUNT 165 a 96 c 126 g 142 t  
ORIGIN

Query Match 9.0%; Score 469; DB 9; Length 529;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GATGACTTTTAAACAGTTTGAAGGATCTAAACATTTGTGTACCTGCAGACATCAATAAGGA 92  
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Db 61 GATGACTTTTAAACAGTTTGAAGGATCTAAACATTTGTGTACCTGCAGACATCAATAAGGA 120  
QY 93 AGAAGAATTTGTAGAAGAGTTTAATAGATTAAAAACTTTTGTCTAATTTTCCAAGTGGTAG 152  
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Db 121 AGAAGAATTTGTAGAAGAGTTTAAATAGATTAAAAACTTTTGTCTAATTTTCCAAGTGGTAG 180  
QY 153 TCCTGTTTCAGCATCAACACTGGCAGCAGGAGGTTCTTTTATCTGTTGAAGGATAC 212  
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Db 181 TCCTGTTTCAGCATCAACACTGGCAGCAGGAGGTTCTTTTATCTGTTGAAGGATAC 240  
QY 213 CGTGCAGTCTTGTAGTTGTCATGAGCTGTAGATAGATGGAATATGAGACTCAGCAGT 272  
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Db 241 CGTGCAGTCTTGTAGTTGTCATGAGCTGTAGATAGATGGAATATGAGACTCAGCAGT 300  
QY 273 TGAAGACACAGAGAAAGTATCCCAAAATTCGAGATTATCAACGGCTTTTATCTTGAAGA 332  
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Db 301 TGAAGACACAGAGAAAGTATCCCAAAATTCGAGATTATCAACGGCTTTTATCTTGAAGA 360  
QY 333 TAGTGCACGAGCTCTACAAATTCGGTATCCAGATGGTCAAGTACAAAGTTGAAAACTA 392  
|||||  
Db 361 TAGTGCACGAGCTCTACAAATTCGGTATCCAGATGGTCAAGTACAAAGTTGAAAACTA 420  
QY 393 TCTGGGAAGCAGAGATCATTTTTCCTCTAGACAGGCCATCTGAGACACATGCAGACTATCT 452  
Db 421 TCTGGGAAGCAGAGATCATTTTTCCTCTAGACAGGCCATCTGAGACACATGCAGACTATCT 480  
QY 453 TTTGAGAACTGGCGAGTTTGTAGATATATATCAGACACCATATACCCGAGG 501  
Db 481 TTTGAGAACTGGCGAGTTTGTAGATATATATCAGACACCATATACCCGAGG 529

RESULT 5	ACCESSION
AL713196	VERSION
LOCUS	
DEFINITION	

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RESULT 6
BM990097/c
LOCUS
DEFINITION
  UI-H-D10-ato-n-20-0-UI.s1 NCI_CGAP_D10 Homo sapiens cDNA clone
  IMAGE:5862355 3', mRNA sequence.
ACCESSION
  BM990097
VERSION
  BM990097.1 GI:19709486
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 691)
AUTHORS
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-re@mail.nih.gov
  Tissue Procurement: Dr. Jose Mercuende
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be found
  through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
  The following repetitive elements were found in this cDNA
  sequence: 11-298, >ALU (matched complement)
  Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
  source
  1. .691
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  /db_xref="taxon:9606"
  /clone="IMAGE:5862355"
  /tissue_type="Lung Focal Fibrosis"
  /dev_stage="Adult"
  /lab_host="DH10B (Life Technologies)"
  /note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
  modified polylinker; Site_1: EcoR I; Site_2: Not I;
  NCI_CGAP_D10 is a cDNA library containing the following
  tissue(s): A pool of Lung Focal Fibrosis. The library was
  constructed according to Bonaldo, Lennon and Soares,
  Genome Research, 6:791-806, 1996. First strand cDNA
  synthesis was primed with an oligo-dr primer containing a
  Not I site. Double stranded cDNA was ligated to an EcoR I
  adaptor, digested with Not I, and cloned directionally
  into p773-Pac vector. The oligonucleotide used to prime
  the synthesis of first-strand cDNA contains a library tag
  sequence that is located between the Not I site and the
  (dr)18 tail. The sequence tag for this library is
  ATACCGGCTC.
  TAG_LIB=UI-H-D10
  TAG_TISSUE=lung with fibrosis
  TAG_SEQ=ATACGGCTC"
BASE COUNT 203 a 177 c 124 g 185 t 2 others
ORIGIN
  Query Match 8.7%; Score 455; DB 14; Length 691;
  Best Local Similarity 99.5%; Pred. No. 0;
  Matches 605; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  QY 4624 GGGTGTAGTGTATATATGATGTTGGCCCTGTGTATATATGATATTTTGTATTTT 4683
  Db 609 GGGTGTAGTGTATATATGATGTTGGCCCTGTGTATATATGATATTTTGTATTTT 550
  QY 4684 TGTCTGTATATTTACATTTTCAGTAGTGTCTTTTGTGTTTCCATTTTAGGGATATA 4743
  Db 549 TGTCTGTATATTTACATTTTCAGTAGTGTCTTTTGTGTTTCCATTTTAGGGATATA 490
  QY 4744 ATTTGTATTTTGAACATATGATGGAGACTACCGCCCGGAGCATTTAGTTTTCACATGATATAC 4803

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|||||
Db 489 ATTTGTATTNTGAACTATGAACTAGGAGACTACGCCGCCAGCATTAGTTTCACATGATATAC 430
QY 4804 CCTTTAAACCCGAATCATTTGTTTATTTTCCCTGATTACACAGGTGTTGAATGGGAAAGG 4863
Db 429 CCTTTAAACCCGAATCATTTGTTTATTTTCCCTGATTACACAGGTGTTGAATGGGAAAGG 370
QY 4864 GCTAGTATATCAGTAGGATATACACTATGGGATGTATATATATATATCATTCCTGTTAGAGAAATG 4923
Db 369 GCTAGTATATCAGTAGGATATACACTATGGGATGTATATATATATATCATTCCTGTTAGAGAAATG 310
QY 4924 AAATAAATGGGCTGGGCTCAGTGGCTACGCCCTGTATATCCAGCACTTTTGGGAGGCTG 4983
Db 309 AAATAAATGGGCTGGGCTCAGTGGCTACGCCCTGTATATCCAGCACTTTTGGGAGGCTG 250
QY 4984 AGGCAGGTGGATCAGCAGGTGAGGAGATCGAGACCATCTCTGGCTAACACGGTGAACACCC 5043
Db 249 AGGCAGGTGGATCAGCAGGTGAGGAGATCGAGACCATCTCTGGCTAACACGGTGAACACCC 190
QY 5044 GTCTCTACTAAAAACAGAAAAATTAGCCGGGCGTGTGGCGGGCGCTGTAGTCCCAGCT 5103
Db 189 GTCTCTACTAAAAACAGAAAAATTAGCCGGGCGTGTGGCGGGCGCTGTAGTCCCAGCT 130
QY 5104 ACTCGGGAGGCTGAGGCGAGGAGATGGTGTGAACCCGGGAGGCGAGCTTGCAGTGAGCC 5163
Db 129 ACTCGGGAGGCTGAGGCGAGGAGATGGTGTGAACCCGGGAGGCGAGCTTGCAGTGAGCC 70
QY 5164 GAGATCTGCCACTGCACCTCCAGCTCGGCAACAGACAGCAAGACTCTGTCTCAAAAAAAA 5223
Db 69 GAGATCTGCCACTGCACCTCCAGCTCGGCAACAGACAGCAAGACTCTGTCTCAAAAAAAA 10
QY 5224 AAAAAAAA 5231
Db 9 AAAAAAAA 2
RESULT 7
BG616695
LOCUS
DEFINITION
  BG616695 537 bp mRNA linear EST 18-APR-2001
  602614908F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4733808 5',
  mRNA sequence.
ACCESSION
  BG616695
VERSION
  BG616695.1 GI:13668066
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
REFERENCE
  1 (bases 1 to 537)
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
TITLE
  National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
  Unpublished (1999)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-re@mail.nih.gov
  Tissue Procurement: CLONETECH Laboratories, Inc.
  cDNA Library Preparation: CLONETECH Laboratories, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  cDNA Sequencing by: Incyte Genomics, Inc.
  Clone Distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LICM1595 row: p column: 01
  High quality sequence stop: 537.
  Location/Qualifiers
  1. .537
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
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  /clone_lib="NIH_MGC_76"
  /lab_host="DH10B (TI phage-resistant)"
  /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
  SfiI (ggccctcgcc); Site_2: SfiI (ggccattggcc); 5' and
  3' adaptors were used in cloning as follows: 5' adaptor

```

sequence: 5'-CACGCCCATTTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCGGCGGACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

BASE COUNT 147 a 81 g 216 t  
ORIGIN

Query Match 8.6%; Score 450; DB 12; Length 537;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4169 CTCACACTCTAATCAAAATTTTGGAGACTTAACAGCATTTGCTGTTGAACATATA 4228  
Db 1 CTCCAACTTCTATCAAAATTTTGGAGACTTAACAGCATTTGCTGTTGAACATATA 60

QY 4229 AAAGCACCAGGATCTTTTCCATCTAATTCGCCAAATAATGATCATTTGCCAAGTCAAAACT 4288  
Db 61 AAAGCACCAGGATCTTTTCCATCTAATTCGCCAAATAATGATCATTTGCCAAGTCAAAACT 120

QY 4289 ATAGCCATATCCAAATCTTTTCCCTCCCAAGAGTCTCAGTGTCTACATGTAGACTAT 4348  
Db 121 ATAGCCATATCCAAATCTTTTCCCTCCCAAGAGTCTCAGTGTCTACATGTAGACTAT 180

QY 4349 TCCTTTTCTGTATAAGTTTCACCTCTAGGATTTCAAGTCCACCACTTATTTTACATTTTAGT 4408  
Db 181 TCCTTTTCTGTATAAGTTTCACCTCTAGGATTTCAAGTCCACCACTTATTTTACATTTTAGT 240

QY 4409 CATGCCAAGATTCAGTAGTTTTCGAATAGTACTTATCTTTATTTGTAATAATTTAGTC 4468  
Db 241 CATGCCAAGATTCAGTAGTTTTCGAATAGTACTTATCTTTATTTGTAATAATTTAGTC 300

QY 4469 TGTGTATCAAAAGCATGCTTAATTTTGGAGAACTGGTTTTCAGATTTTACAACTAAAT 4528  
Db 301 TGTGTATCAAAAGCATGCTTAATTTTGGAGAACTGGTTTTCAGATTTTACAACTAAAT 360

QY 4529 TCAGTGAATTAATTAATAGCTTTATATTCCTTTCCTGCTACATTTGGTTTTCCTCCCT 4588  
Db 361 TCAGTGAATTAATTAATAGCTTTATATTCCTTTCCTGCTACATTTGGTTTTCCTCCCT 420

QY 4589 GTCCCTTTGATTACGGGCTAAGGTAGGGTA 4618  
Db 421 GTCCCTTTGATTACGGGCTAAGGTAGGGTA 450

RESULT 8  
BF510268/c  
LOCUS  
DEFINITION  
UI-H-BI4-api-d-01-0-UI.sl NCI\_CGAP\_Sub8 Homo sapiens cDNA clone  
IMAGE:3087408 3', mRNA sequence.

ACCESSION  
BF510268  
VERSION  
BF510268.1 GI:11593566  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 462)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)

The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Seq primer: M13 Forward  
POLYA=Yes.  
FEATURES  
source  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:3087408"  
/clone\_lib="NCI\_CGAP\_Sub8"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pr773D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not 1; Site\_2: Eco RI; NCI\_CGAP\_Sub8  
is a subtracted library derived from NCI\_CGAP\_Sub5. The  
NCI\_CGAP\_Sub8 library had 2.5 million recombinants. A  
single-stranded DNA preparation of NCI\_CGAP\_Sub5 was used  
as a tracer in a subtractive hybridization with a driver  
comprising: a pool of clones from NCI\_CGAP\_Sub5 (IMAGE  
clone ids 2732833-2737415, 3068040-3069191; 25% of the  
driver population), a pool of clones from NCI\_CGAP\_Sub4  
(IMAGE clone ids 2723592-2729326; 25% of the driver  
population), NCI\_CGAP\_Sub6 (pool AIF-AJU, IMAGE ids  
2728969-2733190; 25% of the driver population), and  
NCI\_CGAP\_Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550  
; 25% of the driver population). Subtraction was  
performed as previously described [Bonaldo, Lennon &  
Soares (1996): Normalization and Subtraction: Two  
Approaches To Facilitate Gene Discovery, Genome Research  
6, 791-806.  
TAG\_LIB=NCI\_CGAP\_Lu5  
TAG\_TISSUE=lung  
TAG\_SEQ=CAAC"

BASE COUNT 172 a 80 c 73 g 137 t  
ORIGIN

Query Match 8.3%; Score 434; DB 12; Length 462;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3725 CCTGTTCTCTGTTTGTAGTATGTAATCCTCAGTTCTTCACCTTTCGACTCTCGCCACTT 3784  
Db 445 CCTGTTCTCTGTTTGTAGTATGTAATCCTCAGTTCTTCACCTTTCGACTCTCGCCACTT 386

QY 3785 AGTTTGTATATAGTCAATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAA 3844  
Db 385 AGTTTGTATATAGTCAATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAA 326

QY 3845 AGTTTGTATATAGTCAATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAA 3904  
Db 325 AGTTTGTATATAGTCAATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAA 266

QY 3905 ACTTCCAAGTCAAGTAGTGTCAATCTAGTTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 3964  
Db 265 ACTTCCAAGTCAAGTAGTGTCAATCTAGTTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 206

QY 3965 GTTTTAAACATAAGGCTTTTCCTGTTCTGGAGCGGCACATTCATTAAATTCCTTCTAAAC 4024  
Db 205 GTTTTAAACATAAGGCTTTTCCTGTTCTGGAGCGGCACATTCATTAAATTCCTTCTAAAC 146

QY 4025 TTGCTATGTTTAGAGTTAAGCAAGACTTTTCTCTCTCCATGAGTCTGAAATTTAA 4084  
Db 145 TTGCTATGTTTAGAGTTAAGCAAGACTTTTCTCTCTCCATGAGTCTGAAATTTAA 86

QY 4085 TGCACACGCTGATGTGGGTAAACAAGTTTATTTTAAAGAATTTGTTTAAAGAATGCTGTGCT 4144  
Db 85 TGCACACGCTGATGTGGGTAAACAAGTTTATTTTAAAGAATTTGTTTAAAGAATGCTGTGCT 26

QY 4145 TCAGGTTCTTAAAA 4158  
Db 25 TCAGGTTCTTAAAA 12

RESULT 9  
BG164322  
LOCUS  
BG164322 943 bp mRNA linear EST 06-FEB-2001

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DEFINITION 602341372F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4449280 5',
            mRNA sequence.
ACCESSION  BG164322
VERSION    BG164322.1  GI:12671025
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 943)
            NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHAM10232 row: p column: 17
            High quality sequence stop: 670.

FEATURES             source
            location/Qualifiers
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:4449280"
            /clone_lib="NIH_MGC_89"
            /tissue_type="hypernephroma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: kidney; vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
            Average insert size 1.3 kb. Library enriched for
            full-length clones and constructed by Life Technologies.
            Note: this is a NIH_MGC Library."
BASE COUNT  297 a  144 c  185 g  317 t
ORIGIN
            1..943
            8.3%; Score 432; DB 12; Length 943;
            Best Local Similarity 99.7%; Pred. No. 0;
            Matches 602; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY  3827 TCTAGACTTTAAATTAAGTTTCTACAGGGGAGAAAGTGTTAAATTTTAAATA 3886
      1 TCTAGACTTTAAATTAAGTTTCTACAGGGGAGAAAGTGTTAAATTTTAAATA 60
      1 TCTAGACTTTAAATTAAGTTTCTACAGGGGAGAAAGTGTTAAATTTTAAATA 60

QY  3887 TGTTCCTCAGGACACTTCACCTCCCAAGTCAGGTAGTTCACATCTAGTTGTTAGCCAA 3946
      1 TGTTCCTCAGGACACTTCACCTCCCAAGTCAGGTAGTTCACATCTAGTTGTTAGCCAA 120
      1 TGTTCCTCAGGACACTTCACCTCCCAAGTCAGGTAGTTCACATCTAGTTGTTAGCCAA 120

QY  3947 GGACTCAGGACTGAATGTTTTACATAAGCTTTTCTGTTCTGGGAGCGGCACTTCA 4006
      1 GGACTCAGGACTGAATGTTTTACATAAGCTTTTCTGTTCTGGGAGCGGCACTTCA 180
      1 GGACTCAGGACTGAATGTTTTACATAAGCTTTTCTGTTCTGGGAGCGGCACTTCA 180

QY  4007 TTAATAATCTCTTAAACTGTATCTTTAGAGTTTAAAGCAAGACTTTTCTCTCTCC 4066
      1 TTAATAATCTCTTAAACTGTATCTTTAGAGTTTAAAGCAAGACTTTTCTCTCTCC 240
      1 TTAATAATCTCTTAAACTGTATCTTTAGAGTTTAAAGCAAGACTTTTCTCTCTCC 240

QY  4067 ATGAGTTGTGAATTTAATGCACACGCTGTATGTGGCTAACAAAGTTATTTTAAAGATTG 4126
      1 ATGAGTTGTGAATTTAATGCACACGCTGTATGTGGCTAACAAAGTTATTTTAAAGATTG 300
      1 ATGAGTTGTGAATTTAATGCACACGCTGTATGTGGCTAACAAAGTTATTTTAAAGATTG 300

QY  4127 TTTAGAAATGCTGTGCTTCAGGTTCTTAAATCACTCAGCACTCCAATCTTAATCAA 4186
      1 TTTAGAAATGCTGTGCTTCAGGTTCTTAAATCACTCAGCACTCCAATCTTAATCAA 360
      1 TTTAGAAATGCTGTGCTTCAGGTTCTTAAATCACTCAGCACTCCAATCTTAATCAA 360

QY  4187 TTTTGGAGACTTACACGATTTGCTGTGTTGAACATATAAAGACCGGATCTTTTC 4246
      1 TTTTGGAGACTTACACGATTTGCTGTGTTGAACATATAAAGACCGGATCTTTTC 419
      1 TTTTGGAGACTTACACGATTTGCTGTGTTGAACATATAAAGACCGGATCTTTTC 419

QY  4247 CATCTAATCCGCAAAAATTTGATCATTTTTGCAAAAGTCAAAACTATAGCCATATCCAAATCT 4306
            CATCTAATCCGCAAAAATTTGATCATTTTTGCAAAAGTCAAAACTATAGCCATATCCAAATCT

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Db  420 CATCTAATCCGCAAAAATAGATCATTTGCAAAAGTCAAAACTATAGCCATATCCAAATCT 479
QY  4307 TTTCCCTCCCAAGAGTTCTCAGTCTACATGTAGACATATTCCTTTCTGTATAAAGT 4366
      1 TTTCCCTCCCAAGAGTTCTCAGTCTACATGTAGACATATTCCTTTCTGTATAAAGT 4366
      1 TTTCCCTCCCAAGAGTTCTCAGTCTACATGTAGACATATTCCTTTCTGTATAAAGT 539
      1 TTTCCCTCCCAAGAGTTCTCAGTCTACATGTAGACATATTCCTTTCTGTATAAAGT 539

QY  4367 TCACCTCTAGGATTTCAAGTCACCACTATTTTACATTTTAGTCATGCAAGATTTCAAGTA 4426
      1 TCACCTCTAGGATTTCAAGTCACCACTATTTTACATTTTAGTCATGCAAGATTTCAAGTA 4426
      1 TCACCTCTAGGATTTCAAGTCACCACTATTTTACATTTTAGTCATGCAAGATTTCAAGTA 599
      1 TCACCTCTAGGATTTCAAGTCACCACTATTTTACATTTTAGTCATGCAAGATTTCAAGTA 599

QY  4427 GTTT 4430
      1 GTTT 4430
      1 GTTT 603
      1 GTTT 603

RESULT 10
AI277821/c
LOCUS      AI277821
DEFINITION qm50e01.x1 Soares_placenta_8to9weeks_2NBHP8to9W Homo sapiens cDNA
            clone IMAGE:1893144 3', mRNA sequence.
ACCESSION  AI277821
VERSION    AI277821.1  GI:39000089
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 472)
            NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 2306 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 438.

FEATURES             source
            location/Qualifiers
            1..472
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            /db_xref="taxon:9606"
            /clone="IMAGE:1893144"
            /clone_lib="Soares_placenta_8to9weeks_2NBHP8to9W"
            /dev_stage="two placenta: one from 8 weeks and another
            from 9 weeks post conception"
            /lab_host="DH10B (ampicillin resistant)"
            /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
            modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st
            strand cDNA was primed with a NotI - oligo(dT) primer [5',
            TGTTACCAATCTGAAGTCGCGGCGGATTTTTTTTTTTTTTTT 3'],
            double-stranded cDNA was size selected, ligated to EcoRI
            adapters (Pharmacia), digested with NotI and cloned into
            the NotI and EcoRI sites of a modified pT7T3 vector
            (Pharmacia). Library constructed by Bento Soares and
            M.Fatima Bonaldo."
BASE COUNT  179 a  83 c  59 g  151 t
ORIGIN
            1..472
            8.1%; Score 422; DB 9; Length 472;
            Best Local Similarity 100.0%; Pred. No. 0;
            Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1540 GTAGGCATGTTATGTTGTTCTTTATACCCTGATTTGAATGATGTGATGTAAGTAA 1599
      1 GTAGGCATGTTATGTTGTTCTTTATACCCTGATTTGAATGATGTGATGTAAGTAA 395
      1 GTAGGCATGTTATGTTGTTCTTTATACCCTGATTTGAATGATGTGATGTAAGTAA 395

QY  1600 GTAATCAGGATTTGAATTTCCATTTAGCATTTGCTTACCAAGTAGGAAAAAATGTACATGGC 1659
      1 GTAATCAGGATTTGAATTTCCATTTAGCATTTGCTTACCAAGTAGGAAAAAATGTACATGGC 1659
      1 GTAATCAGGATTTGAATTTCCATTTAGCATTTGCTTACCAAGTAGGAAAAAATGTACATGGC 335

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QY 1660 AGTGTCTTGGCAATATAATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTAT 1719
Db 334 AGTGTCTTGGCAATATAATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTAT 275
QY 1720 TATCCATTTTTTACTGTATTATTAATGAAACCATAGACTAGAAATAAGACATCATA 1779
Db 274 TATCCATTTTTTACTGTATTATTAATGAAACCATAGACTAGAAATAAGACATCATA 215
QY 1780 CTATACTGAACACAATGTCTATTCATAGTATATCTGATTTAAATTTCTTAAGTGTAAAGTAA 1839
Db 214 CTATACTGAACACAATGTCTATTCATAGTATATCTGATTTAAATTTCTTAAGTGTAAAGTAA 155
QY 1840 TTAATCATCTGGATTTTATCTTTTCAGATAGGCTTAAACAAATGGAGCTTTCTGTATA 1899
Db 154 TTAATCATCTGGATTTTATCTTTTCAGATAGGCTTAAACAAATGGAGCTTTCTGTATA 95
QY 1900 TAAATGTGGAGATTACAGTTAATCTCCCAATCACATAATTTGTTTGTGTAAGAAAGGA 1959
Db 94 TAAATGTGGAGATTACAGTTAATCTCCCAATCACATAATTTGTTTGTGTAAGAAAGGA 35
QY 1960 AT 1961
Db 34 AT 33

RESULT 11
AI299965/c
LOCUS
DEFINITION q024a11.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1909436 3',
mRNA sequence.
ACCESSION AI299965
VERSION AI299965.1 GI:3959311
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 406)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbbrp/image/image.html
Insert Length: 491 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .406
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1909436"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 153 a 74 c 66 g 113 t
ORIGIN
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Query Match 7.8%; Score 406; DB 9; Length 406;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3745 GTAAATCCCTCAGTCTTCACCTTTGCACCTGTCTGCCACTTAGTTTGGTTATATAGTCATT 3804
Db 406 GTAAATCCCTCAGTCTTCACCTTTGCACCTGTCTGCCACTTAGTTTGGTTATATAGTCATT 347
QY 3805 AACTTGAATTTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTCTCAACAGGGGAGAA 3864
Db 346 AACTTGAATTTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTCTCAACAGGGGAGAA 287
QY 3865 AAGTGTAAATTTTAAATATATGTTTCCAGACACTTCACTTCCAAAGTCAGGTAGGTA 3924
Db 286 AAGTGTAAATTTTAAATATATGTTTCCAGACACTTCACTTCCAAAGTCAGGTAGGTA 227
QY 3925 GTTCAATCTAGTTTGTAGCCAAAGGACTCAGGACTGAATTTGTTTACATAGAGCTTTTC 3984
Db 226 GTTCAATCTAGTTTGTAGCCAAAGGACTCAGGACTGAATTTGTTTACATAGAGCTTTTC 167
QY 3985 CTGTTCTGGAGCGGCACCTTCATTAATAATCTTCTTAAACTTCTATGTTTAGAGTTAAGC 4044
Db 166 CTGTTCTGGAGCGGCACCTTCATTAATAATCTTCTTAAACTTCTATGTTTAGAGTTAAGC 107
QY 4045 AAGACTTTTTTCTCTCCATGAGTTGTGAAATTTAATGCACACCGCTGATGGCT 4104
Db 106 AAGACTTTTTTCTCTCCATGAGTTGTGAAATTTAATGCACACCGCTGATGGCT 47
QY 4105 ACAAGTTTATTTAGAATTTTGAATGCTGTGCTTCAGGT 4150
Db 46 ACAAGTTTATTTAGAATTTGTTTGAATGCTGTGCTTCAGGT 1

RESULT 12
AW665401/c
LOCUS
DEFINITION hi90c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2979566 3', mRNA sequence.
ACCESSION AW665401
VERSION AW665401.1 GI:7457948
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 464.
Location/Qualifiers
1. .508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2979566"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH19W, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
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726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " 175 a 89 c 68 g 176 t

BASE COUNT 175 a 89 c 68 g 176 t

ORIGIN

Query Match 7.8%; Score 406; DB 10; Length 508;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 506; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2752 AGTCACTTAAAGATCTTGTAACTCAGTATTTTAAACATCTCTCAGCTTATCTA 2811  
|||||  
Db 508 AGTCACTTAAAGATCTTGTAACTCAGTATTTTAAACATCTCTCAGCTTATCTA 449  
|||||  
Qy 2812 GGTAAAGTAGAAGCATGTTGTACACGCTTGTAGTTATAGTGACAGCTTTCCCATGTTG 2871  
|||||  
Db 448 GGTAAAGTAGAAGCATGTTGTACACGCTTGTAGTTATAGTGACAGCTTTCCCATGTTG 389  
|||||  
Qy 2872 AGATTCTCATATCATCTTGTATCTTAAAGTTTCATGTCAGTTTTPACCGTAGGATGAT 2931  
|||||  
Db 388 AGATTCTCATATCATCTTGTATCTTAAAGTTTCATGTCAGTTTTPACCGTAGGATGAT 329  
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Qy 2932 AAGATGTATATAGGACAAAAGTTTAAAGTCTTCCCTACCTACATTTCTTCTTGGCTA 2991  
|||||  
Db 328 AAGATGTATATAGGACAAAAGTTTAAAGTCTTCCCTACCTACATTTCTTCTTGGCTA 269  
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Qy 2992 GTAATAGTAGATACCTTCTGAAATAAATGTTCTCTCAAGATCCTTAAACCTCTTGG 3051  
|||||  
Db 268 GTAATAGTAGATACCTTCTGAAATAAATGTTCTCTCAAGATCCTTAAACCTCTTGG 209  
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Qy 3052 AATTATAAATAATATGGCAAGAAAGAAAGATAGTTGTTTAAATAATTTTAAAAAACA 3111  
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Db 208 AATTATAAATAATATGGCAAGAAAGAAAGATAGTTGTTTAAATAATTTTAAAAAACA 149  
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Qy 3112 TTGAATAGATCAGTAGGGTATTAACCTAGAGTTTAAATGCTCTATAGAACCTCCAG 3171  
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Db 148 TTGAATAGATCAGTAGGGTATTAACCTAGAGTTTAAATGCTCTATAGAACCTCCAG 89  
|||||  
Qy 3172 GGTTTACATTAACAGATTCTCACACAAACCCATTGTAGAGGTGAGTAGGATCTTACT 3231  
|||||  
Db 88 GGTTTACATTAACAGATTCTCACACAAACCCATTGTAGAGGTGAGTAGGATCTTACT 29  
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Qy 3232 ACAGAGAAAGTTTGAGAGTAAACTGT 3259  
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Db 28 ACAGAGAAAGTTTGAGAGTAAACTGT 1  
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RESULT 13  
BE222433/c  
LOCUS  
DEFINITION hv90g11.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:3180740 3',  
mRNA sequence.  
ACCESSION BE222433  
VERSION BE222433.1 GI:8909751  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 409)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing Arrayed by: Greg Lennon, Ph.D.  
Clone Distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov

Seq primer: -40UP from Gibco.  
Location/Qualifiers  
1. 409  
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/db\_xref="taxon:9606"  
/clone="IMAGE:3180740"  
/clone\_lib="NCI\_CGAP\_Lu24"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Plasmid DNA from the normalized  
library NCI\_CGAP\_Lu5 was prepared, and ss circles were  
made in vitro. Following HAP purification, this DNA was  
used as tracer in a subtractive hybridization reaction.  
The driver was PCR-amplified cDNAs from a pool of 5,000  
clones made from the same library (clones  
1414920-1417991 and 1520904-1522439). Subtraction by Bento  
Soares and M. Fatima Bonaldo. " 155 a 72 c 66 g 116 t

BASE COUNT 155 a 72 c 66 g 116 t

ORIGIN

Query Match 7.7%; Score 405; DB 10; Length 409;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3743 ATGTAAATCCTCAGTTCTTACCTTTGCACTGCTGCCACTTAGTTGCTTATATAGTCA 3802  
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Db 409 ATGTAAATCCTCAGTTCTTACCTTTGCACTGCTGCCACTTAGTTGCTTATATAGTCA 350  
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Qy 3803 TTAACCTTGAATTTGGTGTATAGTCTAGACATTTAAATTTAAAGTTTCTACAAGGGAG 3862  
|||||  
Db 349 TTAACCTTGAATTTGGTGTATAGTCTAGACATTTAAATTTAAAGTTTCTACAAGGGAG 290  
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Qy 3863 AAAAGTGTAAATTTTAAATATATGTTTCCAGGACATTCACCTCCAGTCAGGTAG 3922  
|||||  
Db 289 AAAAGTGTAAATTTTAAATATATGTTTCCAGGACATTCACCTCCAGTCAGGTAG 230  
|||||  
Qy 3923 TAGTTCAATCTAGTTGTAGCCCAAGGACTCAAGGACTGAATTTGTTTAAACATAAGGCTTT 3982  
|||||  
Db 229 TAGTTCAATCTAGTTGTAGCCCAAGGACTCAAGGACTGAATTTGTTTAAACATAAGGCTTT 170  
|||||  
Qy 3983 TCCTGTTCTGGAGCGGCATTCATTAAATTTCTTCTAAACACTTGATGTTTAGAGTTAA 4042  
|||||  
Db 169 TCCTGTTCTGGAGCGGCATTCATTAAATTTCTTCTAAACACTTGATGTTTAGAGTTAA 110  
|||||  
Qy 4043 GCAAGACATTTTCTCTCTCCATGAGTTGTAATTAATGACACACGCTGATGCG 4102  
|||||  
Db 109 GCAAGACATTTTCTCTCTCCATGAGTTGTAATTAATGACACACGCTGATGCG 50  
|||||  
Qy 4103 CTAACAAGTTTATTTTAAAGATTTGTTTGAATGCTGTTGCTTCA 4147  
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Db 49 CTAACAAGTTTATTTTAAAGATTTGTTTGAATGCTGTTGCTTCA 5  
|||||

RESULT 14  
AI681542/c  
LOCUS  
DEFINITION tx47e09.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2272744 3',  
mRNA sequence.  
ACCESSION AI681542  
VERSION AI681542.1 GI:4891724  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 413)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation by: M. Bento Soares, Ph.D.  
DNA Sequencing Arrayed by: Greg Lennon, Ph.D.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 489 Std Error: 0.00  
Seq primer: -40UP from Gibco.

FEATURES  
source  
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/organism="Homo sapiens"  
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/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 154 a 76 c 67 g 116 t  
ORIGIN  
Query Match 7.6%; Score 398; DB 9; Length 413;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3743 ATGTAATCCTCAGTCTTCACCTTTGCCACTGCTGCCACTAGTTGGTATATAGTCA 3802  
Db 413 ATGTAATCCTCAGTCTTCACCTTTGCCACTGCTGCCACTAGTTGGTATATAGTCA 354  
QY 3803 TTAACCTGAATTTGGTCTGTATAGTCTAGACCTTTAAAGTTTCTACAAAGGGGAG 3862  
Db 353 TTAACCTGAATTTGGTCTGTATAGTCTAGACCTTTAAAGTTTCTACAAAGGGGAG 294  
QY 3863 AAAAGTGTAAATTTTAAATATGTTTCCAGGACACTTCACCTCCAAAGTCAGTAGG 3922  
Db 293 AAAAGTGTAAATTTTAAATATGTTTCCAGGACACTTCACCTCCAAAGTCAGTAGG 234  
QY 3923 TAGTCAATCTAGTCTTACGCAAGCACTCAAGGACTGAATGCTTTTAAACATAAGGCTTT 3982  
Db 233 TAGTCAATCTAGTCTTACGCAAGCACTCAAGGACTGAATGCTTTTAAACATAAGGCTTT 174  
QY 3983 TCCTGTTCTGGAGCGCGCACTTCATTAAAAATCTTCTAAAACTGTATGTTTACAGTTAA 4042  
Db 173 TCCTGTTCTGGAGCGCGCACTTCATTAAAAATCTTCTAAAACTGTATGTTTACAGTTAA 114  
QY 4043 GCAAGACTTTTTTCTCTCCATGAGTTGTGAAATTTAATGCAACACGCTGATGTGG 4102  
Db 113 GCAAGACTTTTTTCTCTCCATGAGTTGTGAAATTTAATGCAACACGCTGATGTGG 54  
QY 4103 CTAACAAGTTTATTTTAAAGAAATGTTTAAAGATGCTGT 4140  
Db 53 CTAACAAGTTTATTTTAAAGAAATGTTTAAAGATGCTGT 16

RESULT 15  
BI823020  
LOCUS 603039619F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5180525 5',  
DEFINITION mRNA sequence.  
ACCESSION BI823020  
VERSION BI823020.1 GI:15934570  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 707)  
NIH-MGC http://mhc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabps-re@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11450 row: e column: 06  
High quality sequence stop: 565.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5180525"  
/clone\_lib="NIH\_MGC\_115"  
/lab\_host="DH10B"  
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."

FEATURES  
source

BASE COUNT 204 a 105 c 146 g 252 t  
ORIGIN  
Query Match 7.4%; Score 389; DB 13; Length 707;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 439; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2096 TTTTGAAGCGTATTAAATGATAGAACTATCGAGCCCAACATGTGATGATGGAAGA 2155  
Db 109 TTTTGAAGCGTATTAAATGATAGAACTATCGAGCCCAACATGTGATGATGGAAGA 168  
QY 2156 TGTCAAAGATATCTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCA 2215  
Db 169 TGTCAAAGATATCTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCA 228  
QY 2216 GATCAAAGTATGTATGTTTTTAAATATGATAGCAACAAAGATTTGGAAGATATACACCA 2275  
Db 229 GATCAAAGTATGTATGTTTTTAAATATGATAGCAACAAAGATTTGGAAGATATACACCA 288  
QY 2276 ACTGTGTAATGTGTTCTCTTCGGGGAGGGGGGATTTGGGGAGGGGGCCAGAGGGG 2335  
Db 289 ACTGTGTAATGTGTTCTCTTCGGGGAGGGGGGATTTGGGGAGGGGGCCAGAGGGG 348  
QY 2336 TTTTATAGGGGCTTTTCACTTTCTACTTTTTCATTTTGTCTGTCGAAATTTTTTATA 2395  
Db 349 TTTTATAGGGGCTTTTCACTTTCTACTTTTTCATTTTGTCTGTCGAAATTTTTTATA 408  
QY 2396 AGTATGTTACTTTTGTAAATCAGAAATTTTGAAGAAGTATTTTGTGATTTAAAGCTTA 2455  
Db 409 AGTATGTTACTTTTGTAAATCAGAAATTTTGAAGAAGTATTTTGTGATTTAAAGCTTA 468  
QY 2456 GGCATGTTCAACGGCTCGAAACACTACTATCACTCAGCTTTAGTTTCTTAATCAAGA 2515  
Db 469 GGCATGTTCAACGGCTCGAAACACTACTATCACTCAGCTTTAGTTTCTTAATCAAGA 528  
QY 2516 AGGCAGGGCAGTTAACTTTT 2535  
Db 529 AGGCAGGGCAGTTAACTTTT 548

Search completed: November 10, 2002, 01:30:31  
Job time : 6614 secs



